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APPLICANT: DEROSE, Richard
APPLICANT: CHAUBET, Nicole
APPLICANT: CHAUBET, Nicole
APPLICANT: GIOCO, Claude (decased)
TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
TITLE OF INVENTION: TRANSFORMATION OF PLANTS
TITLE OF INVENTION: TRANSFORMATION OF PLANTS
TILE REPERENCE: 022650-453
CURRENT PRILING DATE: 1996-05-29
EARLIER APPLICATION NUMBER: PT/FR96/01109
EARLIER FILING DATE: 1996-07-17
EARLIER FILING DATE: 1996-07-17
EARLIER FILING DATE: 1996-07-19
NUMBER OF SEQ ID NOS: 22
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100.0%; Score 494; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 2e-128;
Matches 494; Conservative 0; Mismatches 0; Indels
US-10-204-708 41
US-10-204-708-71
US-08-956-171E-244
US-09-816-093-3
US-09-815-093-3
US-09-815-708-10
US-10-204-708-10
US-10-204-708-10
US-09-976-594-760
US-09-134-001C-852
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Patent No. 6338961
GENERAL INFORMATION:
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CORGANISM: Zea mays
US-09-000-062-7
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Sequence 20, Appl
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Sequence 43, Appl
Sequence 55, Appl
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Sequence 28
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( /cgn2 / fptodata/2/ina/5A COMB.seq:*
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): /cgn2 / fptodata/2/ina/6A COMB.seq:*
): /cgn2 / fptodata/2/ina/6A COMB.seq:*
): /cgn2 / fptodata/2/ina/PCTUS COMB.seq:*
): /cgn2 / fptodata/2/ina/PCTUS COMB.seq:*
): /cgn2 / fptodata/2/ina/PCTUS COMB.seq:*
                                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-204-708-29
US-10-204-708-80
US-09-358-082A-29
US-08-956-171E-91
US-09-107-532A-2628
US-10-204-708-62
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US-09-222-463-14
US-08-221-976-2813
US-09-621-976-2813
US-09-621-976-2813
US-09-102-10-204
US-09-10-204
US-08-210-204
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US-09-007-00-17
US-09-007-00-17
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US-08-913-846-8
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US-09-328-352-2881
US-10-204-708-43
US-10-204-708-55
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Maximum Match 100%
Listing first 45 summaries
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10.0%; Score 49.6; DB 1; Length 7218;
Best Local Similarity 6.1%; Pred. No. 0.00022;
Matches 25; Conservative 213; Mismatches 172; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                           APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFRENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ 1D NO: 14:
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: aingle
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                    TCCCGGGATCTGCG 494
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                                                                                                                                                                                                                                                                                                        Patent No. 5670367
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: VA
                                                                                                                                                                                                                                                                            JS-08-232-463-14
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: OLEE, Alexander

APPLICANT: DELEGAN: Alexander

APPLICANT: DELEGAN: Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication

TITLE OF INVENTION: DY ASSESSING DNA Methylation

FILE REFERENCE: 5013.1012 ASSESSING DNA METHYLOGATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR PELING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR PILING DATE: 2000-09-01

PRIOR PILING DATE: 2000-09-01

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-09-01

NUMBER: OF SEQ ID NOS: 98
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                                                                                                                                                                             314 AGGGTTTTCGAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCATCTG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 GGTCTTTCCATTACTTTTAATGTTTTTTCTGTTACTGTCCCGCGATCTGATTTTACGA
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                                                                                                                                                                                                                                                                                   254 TICTGIATAACCAGAITIGICIGIGIGGGAITGICAITACCTAGCCGIGIAICGAGAACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6669;
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7.7%; Score 38.2; DB 4; 1
Best Local Similarity 48.0%; Pred. No. 0.32;
Matches 109; Conservative 0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/10204708
Patent No. 6677731
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NAME/KEY:

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NAME/KEY:

LOCATION: (225001)..(240000)

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NAME/KEY:

LOCATION: (255001)..(270000)

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NAME/KEY: misc feature

LOCATION: (285001)..(300000)

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NAME/KEY: misc feature

LOCATION: (300001)..(315000)

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LOCATION: (300001)..(315000)

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LOCATION: (300001)..(315000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

LOCATION: (300001)..(315000)

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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LOCATION: (105001). (120000)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (120001). (135000)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (135001)..(150000)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (150001)..(165000)
OTHER INFORMATION: n=a or or g or t
NAME/KEY: misc feature
LOCATION: (165001)..(180000)
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NAME/KEY: misc feature
LOCATION: (165001)..(180000)
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NAME/KEY: misc feature
LOCATION: (180001)..(195000)
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NAME/KEY: misc feature
LOCATION: (180001)..(195000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature
LOCATION: (60001). (75000)
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LOCATION: (75001). (90000)
OTHER INFORMATION: n=a or c or g or t NAME/KEY: misc feature
LOCATION: (75001). (90000)
OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (15001)..(3000)
OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or OTHER INFORMATION: n=a or c or g or
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LOCATION: (195001)...(210000)
OTHER INFORMATION: n=a or c or
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
                                                                                                                             TYPE: DNA
ORGANISM: Chlamydia pneumoniae
                                                                                                LENGTH: 1230025
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APPLICANT: Griffais, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 AAGTICTGIAIAACCAGAITIGICTGIGIGGATIGICATTACCTAGCCGIGTATCGAGA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 ACTAGGGTTTTCGAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCAT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 KAWRASCHMRRKYAGKSKISYKSKMWCWIRSWKYCYIKARWIGYYCYRKGGMWGKRGRWY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 371 -CTGGATTAGGGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCTTCAAAATTTAGTTAT 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ASKKYMMKRWWWCWARMYRYSTGTRASMWRRWYYTMMMKWWXYAWARAAWRWWAMWAW 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWAMCWTKRWRAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TGTTTTTCTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRWYWWKYTTWYAKCWTKWKWSWSYWNYWKWYYMKTYWKWRRKKKKKKAMWKYWKTWTWWYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 CCCATTCCAGTTTGAAATAAACGTCCGTCTTTTAAGTTTGCTGGATGATAAACCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                             5359 TGATTİTİTİTİCGIATİTAĞTATİTTİAGTİAGÜGAĞTAİTTATİĞ 5405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
7.5%; Score 37.2; DB 4; Length 832;
Best Local Similarity 9.6%; Pred. No. 0.31;
Matches 35; Conservative 176; Mismatches 154; Indels
                                             230 CATCGTTTTTTTTTGTTGGAAGTTCTGTATAACCAGATTTGTCTG 276
                                                                                                                                                                                                                                        Sequence 2813, Application US/09621976
; Sequence 2813, Application US/09621976
; Sequence 2813, Application US/09621976
; Gaveral No. 663063
; Gaveral No. 663063
; APPLICANT: Dobert, S. APPLICANT: Glochano M.I. S. APPLICANT: Glochano, J.Y.
; APPLICANT: Glochano, J.Y.
; TILE REFERENCE: GENSET.054PR2
; CURRENT APPLICANTON NUMBER: US/09/621,976
; CURRENT FILION DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 2813
; LENGTH: 832
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Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 RRACAA 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 235..399
US-09-621-976-2813
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US-09-198-452A-1
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NAME/KEY: misc feature
LOCATION: (480001)..(495000)
OTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (495001)..(510000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (570001)..(585000)
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NAME/KEY: misc feature NAME/KEY: misc feature LOCATION: (67501)..(690000) OTHER INFORMATION: n=a or c or g or t WE/KEY: misc feature
)CATION: (63001)..(645000)

HER INFORMATION: n=a or c or g or misc feature

WHE/KEY: misc feature

WHE/KEY: (645000) AME/KEY: misc feature OCATION: (660001)..(675000) THER INFORMATION: n=a or c or g or AME/KEY: misc\_feature ACATION: (585501). (600000) THER INFORMATION: n=a or c or g or TAME/KEY: misc\_feature /KEX: misc feature (TION: (46501)..(480000) R. INFORMATION: n=a or c or g or """" misc\_feature Ы О OCATION: (615001)..(630000)
THER INFORMATION: n=a or c or g or WHICH THE TEST OF THE STATE OF LOCATION: (390001)..(405000) OTHER INFORMATION: n=a or c or g or NAME/KEY: misc\_feature LOCATION: (420001). OTHER INFORMATION: n=a or c or g or NAME/KEY: misc\_feature CATION: (600001)..(615000) HER INFORMATION: n=a or c or g NAME/KEY: misc feature LOCATION: (360001)..(375000) OTHER INFORMATION: n=a or c or g LOCATION: (37501)..(39000) OTHER INFORMATION: n=a or c or g NAME/KEY: misc\_feature ION: (405001)..(420000) INFORMATION: n=a or c or g OCATION: (64501)..(660000) THER INFORMATION: n=a or c or NAME/KEY: misc feature LOCATION: (345001)...(360000) OTHER INFORMATION: n=a or c or KEY: misc feature NAME/KEY: misc\_feature NAME/KEY: misc feature LOCATION: (405001)..(42 feature

1130060 APAACTGGGAACTTTPAPAAAGAPATGGAGTTCAGAAAAAGAAAAAAACCTCTTTAT 1130119 1129940 İGAĞTAGAĞAAAİTGIİNAİTITGİTİTÇİNNCAANAİTİTATCITACCAĞİCİÇTI 1129999 1130000 cratridercheaerractreaerecereaaritriracateracitrideaereae 1130059 1130120 TTAATGATTTATTTTTAAAGTATATAAATTAATTAAATTATAAATTAATTTACTTTTT 1130179 1130180 AATAAİTAAAAİÇİAAACTGTİTİĞACİTİAATAAİAİTİATAAİTAİAİAİTTAĞATİTTGAİĞC 1130239 154 GICCGICTITIAAGITIGCTGGAICGAIAAACCIGIGAAGATIGAGICTAGICGAITIAI 213 214 TGGATGATCCATTCTTCATCGTTTTTTTTTTTCGAAGTTCTGTATAACCAGATTTGT 273 274 CTGTGTGCGALTGTCATTACCTAGCCGTGTATCGAGAACTAGGGTTTTCGAGTCAATTTT 333 34 TIAGAICAGGGITTIAGGICTTICCATIACTITTIAAIGTTTTTTCTGTTACTGTCTCCG 0; Gaps 7.5%; Score 37.2; DB 4; Length 1230025; 44.3%; Pred. No. 3.3; tive 0; Mismatches 177; Indels 0; NAME/KEY: misc feature
LOCATION: (765001)..(780000)
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NAME/KEY: misc feature
LOCATION: (780001)..(795000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (795001)..(810000)
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LOCATION: (810001)..(825000)

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LOCATION: (705001)...(720000)
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NAME/KEY: misc\_feature
LOCATICON: (720001)...(735000)
OTHER INFORMATION: n=a or c or g or t 1130240 TTGTCTATTGTTTTGATC 1130257 NAME/KEY: misc feature LOCATION: (750001)..(765000) OTHER INFORMATION: n=a or c or g or 334 GCCCCTTTTGGTTATATC 351 NAME/KEY: misc feature LOCATION: (73501)..(750000) OTHER INFORMATION: n=a or c or g Query Match
Best Local Similarity 44.3
Matches 141; Conservative 8 셤 à 8

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10 AGAACAGGTATGATTTGTAATTAGATCAGGGGTTTAGGTCTTTCCATTACTTTTTA
                                                                                                                                Indels
                                                        Score 36.2; DB 4; 1
Pred. No. 1.1;
0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1740 GATTİTİTİTACGITİTİCGİTTİG 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 CCAATITICITCAAAATITAGITATG 430
                                                                Query Match
Best Local Similarity 43,48;
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-10-204-708-20
US-10-204-708-63
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gequence 63, Application US/10204708
gequence 63, Application US/10204708
gequence 63, Application
general No. 6677731
general INFORMATION:
general INFORMATION:
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general BERLIN, MUMBER: 03,10/204,708
general APPLICATION NUMBER: US/10/204,708
general APPLICATION NUMBER: DE 10019058.8
general BERLING DATE: 2001-04-06
general BERLING DATE: 2000-04-06
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7.5%; Score 37; DB 4; Length 1193;
Best Local Similarity 53.9%; Pred. No. 0.4;
Matches 76; Conservative 0; Mismatches 65; Indels
                                                                                                                            Sequence 23, Application US/09372422A

Sequence 23, Application US/09372422A

Patent No. 633375
GENERAL INFORMATION:
APPLICANT: Reaccis Barrieu
APPLICANT: Reaccis Barrieu
APPLICANT: REACCIS Barrieu
APPLICANT: PELIGNO MAIZE Aquaporins and Uses Thereof
FILE REFERENCE: 0919
CURRENT APPLICATION NUMBER: US/09/372,422A
CURRENT PILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR APPLICATION NUMBER: US 60/098,692
PRIOR FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 23
BEQ ID NO 23
BENOTHMARE: FASTESEQ for Windows Version 3.0
BENOTHMARE: LINGS APPLICATION NUMBER OF SEQ ID NOS: 49
SEQ ID NO 23
BENOTHMARE: PASTESEQ FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGCGATCGAAAACGGCAG 1042
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (88)...(838)

US-09-372-422A-23
                                                                                                                        .09-372-422A-23/c
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Sequence 20, Application US/10204708

Sequence 20, Application US/10204708

Patent No. 6677731

GENERAL INFORMATION:
APPLICANT: DLEX, Alexander
APPLICANT: DLEX, Alexander
APPLICANT: PIEPERROCK, Christian
APPLICANT: BELLIN, Kurt
ITILE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.002
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: US/10/204,708
FRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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                                                                                                                   46 TITAGGICITITCCALTACITITIAAIGITITITICIGITACIGICICCGGGAICIGATITI
                                                                                                                                                                           TYPE: DNA
CRGANISM: Artificial Sequence
FRATURE:
CRCHANISM: Chemically treated genomic DNA (Homo sapiens)
US-10-204-708-20
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Length 5562;
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7.3%; Score 36.2; DB 4; Length 68
Best Local Similarity 45.3%; Pred. No. 1.2;
Matches 208; Conservative 0; Mismatches 248; Indels
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us-09-000-062-7.rni

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5410 Tringrirohriragiririraaacigirgagarranaggraigagirarrarraggri 5469
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GENERAL INFORMATION:
APPLICANT: SEKO, Chisako
APPLICANT: SEKO, Chisako
APPLICANT: KONDO, Tatenya
TITLE OP INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. COMLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5770 TATAGATATAGATAGAAATTTATAGTTGGTTTTTT 5808
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,820
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/835,713
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MEDIUM TYPE: Floppy disk
CMDTUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5512460
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TELEFAX: (617)523-6440
TELEK: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 130 Water Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1493 base pairs
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US-08-340-820-24/c
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1422 İTTITİTGGAALTİLÇIALAARİAARİTİAACITITİTTİRİTİTITITİTİTİTİTİT 1363
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                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 35.8; DB 1; Length 1493; Best Local Similarity 50.3%; Pred. No. 0.92; Matches 88; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHWAN
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Petentin Release #1.0, Version #1.25
SOFTWARE: Petentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMER: US/08/593,535
FILING DATE: 24-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION ADATA:
APPLICATION NUMER: US 07/835,713
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, DAVID G.
REGISTRATION NUMBER: 27026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: NARUO, Ken-ichi
APPLICANT: SEKO, Chisako
APPLICANT: KUROKAMA, Tsutomu
APPLICANT: KONDO, Tatsuya
TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS
TITLE OF INVENTION: PRODUCTION
                                                                                                                                                                ORGANISM: Homo sapiens
HAPLOTYPE: 2n
TISSUE TYPE: skin
CELL TYPE: fibroblast
IMMEDIATE SOURCE:
LIBRARY: Human foreskin cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentr Pc-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-593-535-24/c
; Sequence 24, Application US/08593535
; Patent No. 5622928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION TELEPHONE: (617) 523-3400
                                                                         CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
nucleic acid
EDNESS: double
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                                          TOPOLOGY: linear
MOLECTUE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 We CITY: Boston STATE: Massack COUNTRY: US ZIP: 02109
                     STRANDEDNESS:
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.0283 GITGGIAGGITITIAGGIAGGATTIAGGAGGIAGGIAAGTTATTIAGTTAAGTTATAAG 10342
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        320 TICGAGICAAITITGCCCCTTTTGGTTAIAICTGGTTCGATAACGAITCAICTGGAITAG 379
                                                                                                                                                                                                                                                                                                                                                                   260 ATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCGTGTATCGAGAACTAGGGTT 319
                                                            TGTTACTGTCTCCGCGATCTGATTTTACGACATAGAGTTTCGGGTTTTGTCCCATTCCA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  380 GGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCTAAAATTTAAGTTATGGATAAT 436
                                                                                                                                                           140 GITIGADAATAAACGICCGICITITAAGITIGCIGGAICGAIAAACCIGIGAAGAITGAG
                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
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US-09-007-005-17/c
                                                                 80
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JETCHIC NO. 06.7/31

APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
FILE REFERENCE: 2001-04-06
PRIOR PRILING DATE: 2001-04-06
PRIOR PRILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 TCTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCCATTC 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1362 ratrittracraagaggictrigeciffaagiicacigcgargafacagrgagaa 1308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CAGITIGAAAATAAACGICCGICTITIAAGTITGCIGGATCGATAAACCIGTGAA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.8; DB 1; Length 1493; Pred. No. 0.92; 0; Mismatches 87; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 35; DB 4; Length 10467; Best Local Similarity 44.4%; Pred. No. 2.9; Matches 185; Conservative 0; Mismatches 230; Indels
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORAGNISM: Home sapiens
HAPLOTYPE: 2n
TISSUE TYPE: &kin
CELL TYPE: fibroblast
IMMEDIATE SOURCE:
LIBRARY: Human foreskin cDNA library
CLONE: pGAPI
US-08-593-535-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10204708
Patent No. 6677731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88; Conservative
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Best Local Similarity
Matches 88; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 GITTIGICCCATICCAGITIGAAAATAAACGICCGICTITIAAGITIGCIGGAICGAIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNY
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APPLICANT: SZOGTAK, Jack W.
APPLICANT: SZOGTAK, GARAGE
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE REPRENCE: 00766/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT PILING DATE: 1998-01-14
EARLIER FILING DATE: 1998-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PASESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.0%; Score 34.8; DB 3; Best Local Similarity 11.2%; Pred. No. 1; Matches 27; Conservative 86; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Translation template
Sequence 17, Application US/09007005B Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1) ... (289)
; CTHER INFORMATION: n = A,T,C or US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
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20 TGATTTGTTTGTATAGATCAGGGGTTTAGGTCTTTCCATTACTTTTTAATGTTTTTTC

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FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 GITTITGICCCATICCAGITIGAAAIAAACGICCGICTITITAAGITIGCIGGAICGAIAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 GYCYTYGYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNY 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 TGCTTCGAAGTTCTGTATAACCAGATTTGTCTGTGCGATTGTCATTACCTAGCCGTGT 303
244 IGCTICGAAGIICIGIAIAACCAGAIIIGICIGIGGGAAIIGICAIIACCIAGCCGIGI 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WS-10-204-708-2

Sequence 2, Application US/10204708

Sequence 2, Application US/10204708

Parent No. 667731

APPLICANT: OLEK, Alexander

APPLICANT: DLEK, Alexander

APPLICANT: PIEPERBROCK, Christian

APPLICANT: BIERLIN, Kurt

TITLE OF INVENTION: DY Assessing DNA Methylation

TITLE OF INVENTION: DY Assessing DNA Methylation

FILE REPERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2003-05-06
                         106 NYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYCXAYTYTYGY 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 Trititritritritritritritritraygycygycyayaygyaygyrytyaycyay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                           US-09-244-796-17.
US-09-244-796-17. Application US/09244796

patent No. 6281344

GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
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TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION: PUSIONS
TITLE OF INVENTION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/044,491
EARLIER FILING DATE: 1999-01-04
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PASELEE 1998-01-14

LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 34.8;
11.2%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: (1)...(289)

/ OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 27; Conserva'
                                                                                                                  RESULT 13
US-09-244-796-17/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 TAATGITITICIGITACIGICICCGCGAICTGAITTIACGACAATAGAGITICGGGTIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128 IGTCCCATTCCAGTTTGAAAAAAAACGTCCGTCTTTTAAGTTTGCTGGATCGATAAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.0%; Score 34.4; DB 4; Length 10467; ilarity 45.1%; Pred. No. 4.2; Conservative 0; Mismatches 156; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | Sequence 6, Application US/08913842
| Patent No. 6028250
| GENERAL INVENDATION:
| APPLICANT: TAKAHASHI, Shuichi
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyozo
| APPLICANT: ASADA, Kiyozo
| APPLICANT: RATO, Ikunoshin
| TITLE OF INVENTION: PLANT PROMOTER AND METHOD FOR GENE
| TITLE OF INVENTION: EXPRESSION USING SAID PROMOTER
| NUMBER OF INVENTIORS: 75
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2574 İTATTGİAAAGGIİTATAATTİTİTİTİTİTİTTATATĞİTÄAİ 2617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    248 TCGAAGTTCTGTATAACCAGATTTGTCTGTGTGTGCGATTGTCATT 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 7th Street N.W., Ste. 300 CITY: Washington STATE: D.C. COUNTRY: USA
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PLILING DATE: 2000-04-06
PRIOR PLILING DATE: 2000-04-07
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR PELLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PRILING DATE: 2000-06-30
PRIOR PILLING DATE: 2000-09-01
PRIOR PILLING DATE: 2000-09-01
PRIOR PILLING DATE: 2000-99-01
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                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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APPLICATION NUMBER:
FILING DATE:
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Matches 128; Conserva
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US-08-913-842-6/c
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PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 07-073043
FILING DATE: 30-MAR-1996
FILING DATE: PACKA: 1996
PRIOR APPLICATION NUMBER: PCT/JP96/00777
APPLICATION NUMBER: PCT/JP96/00777
APPLICATION NUMBER: 25.618
ATTORNEY AGENT INFORMATION:
NAME: BROWDY, ROGEL D.
REGISTRATION TOWNER: 25.618
TELEPRAK: (202) 737-3528
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Search completed: June 20, 2004, 05:03:44 Job time: 73.875 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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w model	June 20, 2004, 00:55:23 ; Search time 2930.58 Seconds (without alignments)
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search, 1	20, 2004
nucleic	June
OM nucleic - nucleic search, using sw model	Run on:

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Title: Perfect score: Sequence:	US-09-000-062-6 418 1 tgaggtacgattcttcgatctaatttgttgaacagatccc 418
Scoring table:	IDENTITY NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 08 Maximum Match 1008 Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Listing first 45 summaries	GenBmbl:* 1: gb_ba:* 2: gb_htg:*	9,8,6	g,	ව <sub>ු</sub> පු			) e	e e	 	 	 24: em_ph:*	 	e e e	: em_vi:*	em_htg_	em_htg_	em nrg	34. em_hrg_n]n:*	em htg	em htg	e :	38: em_sy:*
	Database :																					

Pred. No. is the number of results predicted by chance to have a em\_htgo\_hum:\* em\_htgo\_mus:\* em\_htgo\_other:\* 

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2 (bases 1 to 4833)
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TITLE
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1 (bases 1 to 418)

1 (bases 2 to 418)

DeRose,R., Chaubet,N. and Gigot,C.

1solated DNA sequence capable of serving as regulatory element in a chimeric gene which can be used for the transformation of plants

Patent: US 6338961-A 6 15-UAN-2002;

Location/Qualifiers
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100.0%; Score 418; DB 6; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.1e-81;
Matches 418; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                   Length 418;
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GENE USEFUL FOR TRANSFORMING PLANTS
Patent: WO 9704114-A 6 06-FEB-1997;
RHONE POULENC AGROCHMIE (FR)
Other publication FR 273629 970124.
Location/Qualifiers
1. 418
/ crain="Rrabidopsis thaliana"
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al Similarity 100.0%; Score 418; DB 6;
al Similarity 100.0%; Pred. No. 2.1e-81;
418; Conservative 0; Mismatches 0;
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Sequence 6 from patent US 6338961.
AR182671
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AR182671
                           JOURNAL
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ATH3G
A.thaliana H3 gene 1 and H3 gene 2 for H3.3-like histone variant.

NA 6.0429
NA 6.0429.1 GI:16323
Asione, histone H3.3 homologue.

Arabidopsis thaliana (thale cress)
LSM Arabidopsis thaliana (thale cress)
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 4833)
Chaubet, N., Clement, B. and Gigot, C.
Genes encoding a histone H3.3-like variant in Arabidopsis contain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gigot, C.
Direct Submission
Submitted (17-SEP-1991) C. Gigot, Inst de Biologie Mol des Plantes, Submitted (17-SEP-1991) C. Gigot, Inst de Biologie Mol des Plantes, 12 Rue du General Zimmer, 67084 Strasbourg Cedex, FRANCE
Location/Qualifiers
                                                                                                                                                                                                                                                                                                 TITCITGATIATGCGALTGCAATTAGGGATTTTCTTTTGGTTTTGTGTTGATCTTACGATA 360
                                                                              120
                                                                                                             61 AACTACTGGAATCGCTCGATAGGTGGTACGAATTAGGCGAGATTAGTTTCTATTCTTGG 120
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1 TGAGGIACGATICTTCGATCCTCTTTGATTTTCCTGGAAATATTTTTCGGTGATCGTGA
                                                                            AACTACTGGAATCGCTCGATAGGTGGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGG
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/ Organism="Arabidopsis thaliana"
/ mol type="Genomic DNA"
/ strain="Columbia"
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/ coll line="Columbia"
/ clone lib="cosmid c22"
/ dev stage="callus"
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J. Mol. Biol. 225 (2), 569-574 (1992)
92277663
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ATCHRIV92 112067 bp DNA linear PLN 16-WAR-2000
Arabidopsis thaliana DNA chromosome 4, contig fragment No. 92.
AL161596
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 107700)
Murphy,G., Ridley,P., Hudson,S., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
Unpublished
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EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

Submitted ("MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
                                                                                                                                                                                                                                                                                                                                   09
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Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W.,
Lemcke, K. and Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .... (Dass. 107578 to 112067)
Rose, M., Hempel, S., Entian, K.-D., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
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                                                                                                                                                                                                                                        Length 4833;
                                                                                                                                                                                                                                          Query Match 99.3%; Score 415; DB 8; Length 48 Best Local Similarity 100.0%; Pred. No. 7.1e-81; Matches 415; Conservative 0; Mismatches 0; Indels
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HPRRRPPTSESSNIVPEWNDTRSRLÄÖSLAIKARRGFIHALPENSDKVIVLLNTQNEV
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VSSLPSSIMGCGQIKR"
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre. Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
Information operformance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thai/this fragment has an overlap with ATCHRIV91 at the 5' end and an overlap with ATCHRIV91 at the 5' end and an overlap with ATCHRIV91 at the 5' end and an overlap with ATCHRIV91 at the 5' end and an overlap.
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Contains Glycosyl hydrolases family 5 signature
AA384-393;Multicopper oxidases signatures
AA31-151;Multicopper oxidases signatures
AA540-560;Multicopper oxidases signatures
AA540-556;Prokaryotic membrane lipoprotein lipid
attachment site AA567-577
contains EST gb:A1994215.1, AA585817, A1996008.1"
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MVSLL"
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GASSI I APSLRHLI ORLALGWRI RLI OHLLRNYLRNNAFYKVFHMSGNS I DADORLI R
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number=5
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Jelus. 26772

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                         Mayer, K.F.X., Lemcke, K. and Schueller, C.

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Lose 118267)

SE Varabidopsis sequencing, project.

Blirect Submission

Direct Submission

National Coloration

AL Sibonemie, Am Klopferspitz 18a, D-82152 Martinstidut fuer

Submitted (21-SED-1999) MIPS, at the Max-Planck-Institut fuer

Submitted (21-SED-1999) MIPS, at the Max-Planck-Institut fuer

Schuell-demips blochem img. de_mayer@mips. blochem.img. de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael-bevan@bbsrc.ac.uk

Coordinaton of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.

S Location/Qualifiers

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22854. .24209
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Arabidopsis thaliana DNA chromosome 4, BAC clone T5/17 (ESSA
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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98.5%; Score 411.8; DB 8; Length 112067;
Best Local Similarity 99.5%; Pred. No. 2.4e-80;
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Best Local Similarity 47.8%;
Matches 151; Conservative
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            Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune system
Diagnosis of diseases associated with the immune system
Diagnosis of Guesta 1607 03-JAN-2002;
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CATTCCTGCAATTGAATACGTATGGATCTAAATCTTGTTAATTTGTTGAACAGAT 415
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Best Local Similarity 49.7%; Pred. No. 0.045;
Matches 165; Conservative 0; Mismatches 166; Indels 1.
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                                                                                            AX346536 5998 bp DNA Sequence 1607 from Patent W00200928.
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Sequence 12 from Patent WO0200932.
AX344561
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                                                                   RESULT 6
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Plasmodium falciparum 3D7

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (basea; Lo 253151)

Gardner, M. J. Hall, N., Fung, E., White, O., Berriman, M., Hyman, R.W., James, K., Eisen, J.A., Rutherford, K., Sowman, S., Paulsen, I.T., James, K., Eisen, J.A., Rutherford, K., Salzberg, S.L., Craig, A., Kypici, S., Nane, V., Shallom, S.U., Suh, B., Pererson, J., Angiuoli, S., Perrea, M., Allen, J., Selangut, J., Haft, D., Mather, M.W., Vaidya, A.B., Martin, D.M.A., Fairlamb, A.H., Frannholz, M., Subramanian, G.M., Mungall, C., Venter, J.C., Cummings, L.M., Subramanian, G.M., Mungall, C., Davis, R.W., Fraser, C.M. and Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
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                                                                                                                                                                                                                                                                                               98 GCGAGATTAGTTTCTTTGCCCATTATCTTGTTTCTTCGCCGAATGATCTTCCGTAT
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                                                                             Gaps
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Score 52; DB 6; Length 349980; Pred. No. 0.091; 0; Mismatches 165; Indels 0
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Barrell, B. TITLE Genome sequence of the human malaria parasite Plasmodium falciparum JONENAL Nature 419 (6906), 498-511 (2002) PUBMED 12368864 REPERBNC 2 (bases 1 to 253151)		rce	/isolate="3D7" /db_xref="taxon:36329"	/Chromosome=11" repeat_region complement(73101)	/rpt type=tandem /rpt type=tandem repeat region 173279		repear_region (note="father") / note="father" / reft type=faindem / reft type=faindem	/rpt_type=tanden /rpt_unit="(TA)"		repeat_region 545578		/rpc_cype=candem /rpc_unic="(TA)n reneat region complement(580673)	/note="AT_rich" /rpt_type=tanden	repeat_region 762795 /rpt_type=tandem	/rpt_type=tandem /rpt_unit="(TA)r	complement (869. /note="AT_rich" /rpt_type=tandem	repeat_region complement(9569/5) /rpt_type=tandem /rpt_unit="(A)n"	repeat_region complement(9831040) /note="AT_rich" /rpt type=tandem	repeat_region 1094.il21 /rpt_type=tandem /rpt_inst_r="(a)n"	ment (: "AT_r:	/rpt_type=tandem repeat_region 1299139 .	Tement (	/rpt_unle="(1A,n" repeat_region complement(13231379) /note="AT_rich"	/rpt_type=tandem repeat_region complement(15711605) /nore="AT rich"	/rpt_type=tandem repeat_region complement(1621. 1699) /note="AT_rich"

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                                                                                                                                                                                                                                                                                                                                                                           312 IGCGATIGCAATIAGGGATTTICTTIGGTTTTGTGTTGATCTTACGATACATICCTGCAA 371
                                                                                                                                                                                                                                                                                                                                           1. .17527
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/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                            252 TGTGTAAATAGATTGTTCTTATTCGGCGATTGTTGATTAGGGTTTTGATTTTCTTGATTA
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1405 03-JAN-2002;
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                                                                                                                                                                            Length 17527;
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Diagnosis of diseases associated with metabolism Patent: Wo 0.17645.A. 27 18-OCT-2001;
Epigenomics AG (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGAATACGTATGGATCTAAATCTTGTTAATTTGTTG 408
                                                                                                                                                                            Query Match 12.1%; Score 50.6; DB 6; 1
Best Local Similarity 52.1%; Pred. No. 0.27;
Matches 113; Conservative 0; Mismatches 104;
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Seguence 1405 from Patent W00200928.
AX346334
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Location/Qualifiers
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12.2%; Score 51.2; DB 3; Length 253151;
Best Local Similarity 49.6%; Pred. No. 0.14;
Matches 131; Conservative 0; Mismatches 133; Indels 0;
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Sequence 27 from Patent WO0176451.
AX339160
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4163, .4226
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Gaps

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BX470257 206653 bp DNA linear HTG 24-SEP-2003 Danio rerio clone DKEY-99015, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                  5490 GAGTITCGGITCGAGGGGTATAGTATGGTTAGATTTAGTGATTAATTTGTTTTTAGGTAG 5549
                                                                                                                                                                                                                  irinininintarininintarinintarinintarinintarinintarinintarinintarin 5729
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                                                                                          161 GATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCT 220
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Submitted (24-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonesequest@sanger.ac.uk
On Sep 24, 2003 this sequence version replaced gi:32169046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                            221 AGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTCTTATTCGGCGA
                                                                                                                                                                                                                                                         281 TIGITGATTAGGGTTTTGATTTCTTGATTATGCGATTGCAATTAGGGATTTTCTTTGGT
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 205905 bases at least Q40
Consensus quality: 206063 bases at least Q40
Consensus quality: 206063 bases at least Q30
Consensus quality: 206151 bases at least Q20
Insert size: 206253; unn-of-contigs
Insert size: 198710; 1.2% error; agarose-fp
Quality coverage: 7.80x in Q20 bases; sum-of-contigs Quality
coverage: 8.14x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record usl be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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0
           Length 6306;
        12.0%; Score 50.2; DB 6; Length 6 llarity 50.2%; Pred. No. 0.37; Conservative 0; Mismatches 123; Indels
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BX470257.3 GI:35209325
HTG, HTGS PHASE1; HTGS_EULLTOP.
Danio rerio (zebrafish)
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                                                                                               PAT 01-NOV-2001
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db xrefe"-txxon:35450"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with dna transcription
Patent: WO 0192565-A 331 06-DEC-2001;
Epigenomics AG (DE)
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                                                                                                                                                                                                                                                                                    Olek, A., Piepenbrock, C. and Berlin, K.
Diagnosis of diseases associated with gene regulation
Patent: WO 017375-A 223 18-OCT-2001;
Epigenomics AG (DE)
Location/Qualifiers
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                                                                                                   AX278060 6306 bp
Sequence 223 from Patent WO0177375.
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AX278060.1 GI:16605132
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Apis mellifera clone CH224-59E13, *** SEQUENCING IN PROGRESS ***,
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AC141780.1 GI:29123964
AC141780.1 GI:29123964
APIG, HTGS PHASE1.
Apis mellifera
Apis mellifera
Bukaryota; Metazaa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Mymenoptera; Apocrita; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 TITAGGITAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGA 223
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11.9%; Score 49.6; DB 2; Length 206653;
Best Local Similarity 47.7%; Pred. No. 0.33;
Matches 145; Conservative 0; Mismatches 159; Indels 0;
966 65065: gap of 100 bp

066 83771: contig of 18706 bp in length

772 83871: gap of 100 bp

873 137062: gap of 100 bp

063 187052: contig of 49639 bp in length

756 186855: gap of 100 bp

756 186855: gap of 100 bp

186852 gap of 100 bp

186852 app of 100 bp

186852 app of 100 bp

186852 app of 100 bp
                                                                                                                                                                                                                                                                                                                                                     /organism=Danio rerio"
/mol type="genomic DNA"
/db_xref="taxon:7955"
/dlone="DREY-99015"
/clone="brefy="banioRey"
1. 64966
/note="assembly fragment:03254
fragment_chain:1"
65066. 33771
/note="assembly fragment:01800
fragment_chain:1"
83772. 136962
/note="assembly fragment:02854
fragment_chain:1"
137063. 136962
/note="assembly fragment:02854
fragment_chain:1"
137063. 186755
/note="assembly_fragment:0600.0"
186856. 206653
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                        1115: contig of 1115 bp in length 1215: gap of unknown length 2262: contig of 1047 bp in length 2362: contig of 1047 bp in length 3978: contig of 1616 bp in length 4078; gap of unknown length 5245: gap of unknown length 6792: contig of 1067 bp in length 6792: gap of unknown length 6792: gap of unknown length 8155: contig of 1363 bp in length 8155: gap of unknown length 9553: gap of unknown length 11773: gap of unknown length 11773: gap of unknown length 11773: gap of unknown length 11273: gap of unknown length 11273: gap of unknown length 1278: contig of 1410 bp in length 1278: gap of unknown length 14171: contig of 1834 bp in length 14177: contig of 1834 bp in length 14771: gap of unknown length 14771: contig of 1834 bp in length 14771: contig of 1834 bp in length 14771: contig of 1834 bp in length 14771: contig of 1834 bp in length
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67129: contig of 3001 bp in length
67229: gap of unknown length
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70167: contig of 2383 bp in length
70167: gap of unknown length
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70167: contig of 3260 bp in length
70167: gap of unknown length
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80255: contig of 3130 bp in length
80255: contig of 3190 bp in length
80255: contig of 2919 bp in length
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80241: contig of 2919 bp in length
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80241: contig of 4559 bp in length
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80242: gap of unknown length
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80245: contig of 4559 bp in length
802711298: contig of 4339 bp in length
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Best Local Similarity 52.0%; Pred. No. 0.42;
Matches 132; Conservative 0; Mismatches 120; Indels
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/mol type="genomic DNA"
/db_xref="taxon:7460"
/clone="CH224-59Bl3"
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Best Local Similarity 45.2%; Pred. No. 0.37;
Matches 180; Conservative 0; Mismatches 218; Indels 0; Gaps
                         Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of known genetic parameters within the mhc
Patent: WO 0200932A 24 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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Job time : 2934.58 secs
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1 tgaggtacgattcttcgatc......taatttgttgaacagatccc 418
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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SUMMARIES	AATES996 ABL33634 AASG3343 AASG3343 AASG3343 AASG45515 ABK34857 ABBA1307 AABK39964 ABK29966 ABK29966 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK29976 ABK39990 ABK39990 ABK34536 ABK34536
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ABLJ33999 ABLJ4295 ABC18144 ABC18144 ABC18145 ABLJ34564 ABLJ70289 ABLJ34595 ABLJ3495 ABLJ32509 ARZ0253 AAX20253 AAX202384 ABK4008 ABL32649 ABK4008 ABL3262 AAX41736 AAX41736	ABQ20161 ALIGNMENT	въ.			H3.3-like	tion sequence; intr enolpyruvylshikimat		lifiers					IIMIB.	, O;		chimeric at least resistan	ıch.	122 of Arabidorion of clone c2 in generated a fragment, designating into pla
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for

Nucleic acid comprising fragment of chemically modified gene, useful idiagnosis and treatment of diseases associated with abnormal cytosine

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Berlin

Piepenbrock C,

olek A,

WPI; 2002-130909/17

methylation.

(EPIG-) EPIGENOMICS AG

Claim 1; SEQ ID NO 1607; 32pp + Sequence Listing; German

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to the intron 1 sequence, the vectors contained a plant promoter and a herbicide tolerance gene (e.g. a mutated version of the 5-enolpyruvylshikimate-3-phosphate synthase (BPSPS) gene). The intron enhances expression of the herbicide tolerance gene in rapidly growing parts of plants. The intron can also be used to enhance expression of genes that impart resistance to pathogens or that encode nutritional or therapeutic proteins
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                                                                                                                        Sequence 418 BP; 100 A; 63 C; 85 G; 170 T; 0 U; 0 Other;
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                                                                                                                                                    100.0%; Score 418; DB 2; 100.0%; Pred. No. 2.8e-92;
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01-SEP-2000; 2000DE-01043826.
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Best Local S:
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid returamine, Alzheimer's disease, Alzheipsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antillammatory; cancer; eye arteriosolerosis; anaemia;
acute myeloid leukaemia; Albieimer's disease, AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                                                                                                                                                                       6; Length 5998;
                                                                                                                                                                                                                                                  13.0%; Score 54.4; DB 6; Length 5 49.7%; Pred. No. 0.0013; ive 0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 1405.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4682 TATGGGATTATTTTTTTTTTTATGTTTTAG 4713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 TACGTATGGATCTAAATCTTGTTAATTTGTTG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL33432 standard; DNA; 17527
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                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 49.7
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases of a segment of the chemically pretreated DNA of genes casociated with metabolism such as DUSPS (NM 000120), SGSH (NM 000199), SHWIZ (NM 000121), SIC7A2 (NM 000120), SGSH (NM 000199), SHWIZ (NM 000112), SIC7A2 (NM 000120), SIC7A4 (NM 000120), SHWIZ (NM 001011) (all undefined). (I) care useful for diagnosis and therapy of metabolic disease, solid tumours and cancers, as primer oligonuclecides for the amplification of DNA sequences, for detecting the cytosine methylation state and/or single conclectide polyworphisms (SNPS) in a chemically treated DNA Genes associated with metabolism. An array of (I) is useful for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases by analysing cytosine methylations. The method involves chemically treating genomic cytosine methylations. The method involves chemically treating genomic oversine methylations are unmethylations. The method involves chemically pretrated genomic DNA. The genomic DNA is from call or another base which is dissimilar to cytosine in terms of hybridisation behaviour and amplifying fragments of the converted to uracil or another base which is dissimilar to cytosine in the components which contain DNA, sources of DNA comprising, for cellular components which contain DNA, sources of DNA comprising, for cellular insertions, deletions, point mutations, inversions and contine of business of genes associated with metabolism entity and futher combinations. Genetic parameters are in particular cytosine methylations and further chemical modifications of DNA bases of genes associated with metabolism. Further epigenetic parameters include Gor their regulation of Bistomes which correlates are in particular cytosine methylations and further chemical methylations of DNA solices of the involvance of the involvance of the involvance of the involvance of the involvance of the involvance of the involv
                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid, useful for diagnosis and therapy of metabolic disease, solid tumor and cancers, comprises segment of chemically modified genomic sequences of genes associated with metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 79-84; 143pp; English
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                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                        06-APR-2000; 2000DE-01019058.
                                                                                                                             07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                 06-APR-2001; 2001WO-EP004016
                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
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18-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid theumantoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312 IGCGATTGCAATTAGGGATTTTCTTTTGTGTTTGATCTTACGATACATTCCTGCAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytostatic, anti-tumour, metabolism, metabolic disease, liver, solid tumour, cancer; cytosine methylation, epigenetic; eye; kidney, single nucleoride polymorphism detection, SNP, stool; urine; lung; cerebral-spinal fluid; intestine; brain; heart; prostate; breast; DUSP2; EPHX2; QDPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 TGTGTAAATAGATTGTTCTTATTCGGCGATTGTTGATTAGGGTTTTGATTTCTTGATTA
                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified gene, useful i
diagnosis and treatment of diseases associated with abnormal cytosine
methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 GATTTCATCACCAGATAGTTTCTTTGTCTAGAATCTCTGAAATTCTCGATAGTTTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17527 BP; 4501 A; 296 C; 4094 G; 8636 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 50.6; DB 6; Length 17527; 52.1%; Pred. No. 0.013; cive 0; Mismatches 104; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1405; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemically pretreated metabolism associated gene #27.
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                                                                                                                                                                                                                                                                                                         Berlin K;
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                                                                                                                                                                30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                              02-JUL-2001; 2001WO-EP007537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52.1
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130909/17
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     WO200200928-A2
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                                                             03-JAN-2002
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16590 GTTGTTATAAGAATATTTTGTTTTTTTTGAGTCGTTATTATTTTAGAAAGTTTTAAGA 16649
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                                                                                                                                                                                                                                                                                                                192 GATTICATCACCAGATAGTTTCTTTGTCTAGAATCTCTGGAAATTCTCGGATAGTTTTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 IGIGIAAAIAGAIIGIICIIAIICGGCGAIIGIIGAIIAGGGIIIIIGAIIIICIIGAIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 IGCGATIGCAATIAGGGATTTTCTTTGGTTTTTGTGTTGATCTTACGATACATTCCTGCAA
                                                                                                                                                                                                                          0;
                                                                              Sequence 17527 BP; 4501 A; 296 C; 4094 G; 8636 T; 0 U; 0 Other;
                                                                                                                                                        DB 6; Length 17527;
                                                                                                                                                    Query Match 12.1%; Score 50.6; DB 6; Length 1
Best Local Similarity 52.1%; Pred. No. 0.013;
Matches 113; Conservative 0; Mismatches 104; Indels
associated genes, and related primers of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGAATACGTAIGGAICTAAAICTIGTIAATTIGGTIG 408
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RESULT 4

16770 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTAG 16806

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Cell cycle; human, CpG dinuclectide, cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                          Chemically pretreated complementary DNA associated with cell cycle #110.
                                                                                                                                                                                                                                                                                                                                                                                                                     Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
          AAS45515 standard; DNA; 6306 BP
                                                                                                                                                                                                                                                                                         2000DE-01019058.
2000DE-01019173.
2000DE-01032529.
                                                                                                                                                                                                                                                                                          06-APR-2000; 2000DB-01019058.
07-APR-2000; 2000DB-0101173
30-JUN-2000; 2000DB-01043826.
01-SEP-2000; 2000DB-01043826.
                                                                                                                                                                                                                                                        15-MAR-2001; 2001WO-EP002945
                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with cell cycle.
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-602751/68.
                                                                                                                                                                                                          WO200168911-A2
                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                15-MAR-2000;
                                                        18-DEC-2001
                                                                                                                                                                                                                                   20-SEP-2001
                                                                                                                                                               PCR primer
                                   AAS45515;
AAS455
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Berlin K;

Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated NRA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, activiscalentary graft of the contract of the disease, activities, adjing, glomerular disease, Lewy body disease, arthritis, Claim 1; SEQ ID NO 220; 28pp; English.

Gaps ö Sequence 6306 BP; 1455 A; 190 C; 1580 G; 3081 T; 0 U; 0 Other; Score 50.2; DB 4; Length 6306; Pred. No. 0.014; 0; Mismatches 123; Indels 0; Query Match Best Local Similarity 50.2%; Matches 124; Conservative

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5549 5490 GAGTTTCGGTTCGAGGGGTATAGTATGGTTAGATTTAGTGATTAATTTGTTTTAGGTAG 161 GATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCT

ò d 221 AGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTCTTATTCGGCGA 280

The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligomicleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase

Claim 1; SEQ ID NO 331; 32pp; English.

5670 irinininahirinnininninninganninnintrinninninninninninnin 5729 DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurological disorder; erythropoiesis; myelodysplastic syndrome; myenchourg syndrome; Niemann-Pick disease; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour. New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumors or TITGIGITGAICTIACGAIACAIICCIGCAATIGAAIACGIAIGGAICTAAAICTIGITA TIGITGATTAGGGTTTTTGATTTTCTTGATTATGCGATTGCAATTAGGGATTTTCTTTGGT rgaritraettritritggrgggrtitratararcgrtitrrrrrrrrrrrrrrrrrrrrr DNA transcription associated genomic DNA #166. Berlin K; ВЪ 2000DE-01019173. 2000DE-01032529. 2000DE-01043826. ABK28457 standard; DNA; 6306 06-APR-2001; 2001WO-EP003973 (first entry) Olek A, Piepenbrock C, Ä 401 ATTIGIT 407 (EPIG-) EPIGENOMICS WPI; 2002-090046/12. 5730 TTTTTT WO200192565-A2 07-APR-2000; 30-JUN-2000; 01-SEP-2000; Unidentified. 06-APR-2000; 23-APR-2002 06-DEC-2001 5610 341 ABK28457; 281 cancer RESULT 6 ABK28457 ò g ò 셤 ठ

us-09-000-002-6.rng

deficiency, viral infection, retroviral infection, Sezary syndrome, haematological disorders, immunological disorders, Werner syndrome, ruberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Maardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial infarction, hypertension, angiogenesis, erythropoiesis, congenital heart disease, HDR syndrome, arthritis, polydiutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from the European Patent 8888888888888888

Sequence 6306 BP; 1455 A; 190 C; 1580 G; 3081 T; 0 U; 0 Other;

ö Gaps ô DB 6; Length 6306; 12.0%; Score 50.2; DB 6; Length 6 50.2%; Pred. No. 0.014; cive 0; Mismatches 123; Indels Matches 124; Conservative Query Match Best Local Similarity

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5490 gagitircedirceaegegialaegialeetraeatitaeleartaatitichititaeelae 5549 161 GATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCT 220 221 AGARICTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTCTTATTCGGCGA TIGITGATTAGGGTTTTGATTTTCTTGATTATGCGATTGCAATTAGGGATTTTCTTTGGT

401 ATTTGTT 407

5730 Tririri 5736

ABL33562 standard; DNA; 5987 BP.

(first entry) 26-MAR-2002 Human immune system associated gene SEQ ID NO: 1535.

Human; immune system disease; cytosine methylation; antiasthmatic; antianteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; 

Homo sapiens

03-JAN-2002

02-JUL-2001; 2001WO-EP007537 30-JUN-2000; 2000DE-01032529. 01-SEP-2000; 2000DE-01043826.

(EPIG-) EPIGENOMICS

Berlin Piepenbrock C, olek A,

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3092 2912 2972 3032 3152 347 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, atteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheipsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention 287 407 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine TITCIATICITGGCCATIATCITGTITCTTCGCCGAATGATCTTCCGTATAAAGATTTTA 2853 TITITITITATGITIAGATTIGIATTTTTITAAAATTITGITTAAAAGTTITA GGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCT 2973 GITATATATAGATAGAATITITATTATGGGATAGATGGAGTTTAATITITTTGAGTTTA 288 TTAGGGTTTTGATTTCTTGATTATGCGATTGCAATTAGGGATTTTCTTTGGTTTTGTGT TGATCTTACGATACATTCCTGCAATTGAATACGTATGGATCTAAATCTTGTTAATTTGTT 228 CIGAAAIICICGAIAGIIIICACAIGIGIAAAIAGAIIGIICIIAIICGGCGAIIGIIGA 2913 GAPPTTTTTGAAPTTTTTTTTTTTTTAAGTATATGGAAFTTTTTTATTTT . 0 Sequence 5987 BP; 1754 A; 96 C; 1096 G; 3041 T; 0 U; 0 Other; Query Match 11.7%; Score 49; DB 6; Length 5987; Best Local Similarity 47.5%; Pred. No. 0.026; Matches 145; Conservative 0; Mismatches 160; Indels Claim 1; SEQ ID NO 1535; 32pp + Sequence Listing; German 3153 TAAAA 3157 WPI; 2002-130909/17 GAACA 412 methylation. 348 408 108 168 셤 d 셤 à g ò ద ò ઠ à ઠે g

ABQ67101 standard; DNA; 5987 

28-AUG-2002 (first entry)

Human angiogenesis associated polynucleotide SEQ ID NO 131.

Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.

Ношо

WO200246454-A2

06-DEC-2001; 2001WO-EP014320.

WO2003072821-A2

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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (AB666511-AB671148) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, necvascular glaucoma, solid tumours, inflammation, rheumatoid architis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and crown's diseases. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                   New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. diagnosis or treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5987 BP; 1754 A; 96 C; 1096 G; 3041 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                      claim 1; SEQ ID NO 131; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 47.5%;
Matches 145; Conservative (
06-DEC-2000; 2000DE-01061338.
                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                   WPI; 2002-500450/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                            Schacht O;
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3093 İTTİTTAĞAİAATAGAAİAATTAATGTİTGAİAAĞĞAĞA AAİAĞAİĞAİĞAİTATİİ 3152 2973 GİTATAİAAGTGAİAGAAİİTTTAİTTATGGGAİAĞAİGGAGTİTAAİTTTTTTGAĞİTTA 3032 trintritaricantacentriciaritariantarakantariantarianka 2912 ö 288 TTAGGGTTTTGATTTTGTTATGCGATTGCAATTAGGGATTTTCTTTGGTTTTGTGT 347 407 TITCIAITCTIGGCCATTAICTTGTTTCGCCGAATGATCTTCCGTATAAGATTTTA 167 CIGAAATICICGAIAGITITICACAIGIGIAAAIAGAITGITCITAITCGGCGAITGITGA 287 GGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCT 348 TGATCTTACGATACATTCCTGCAATTGAATACGTATGGATCTAAATCTTGTTAATTTGTT Score 49; DB 6; Length 5987; Pred. No. 0.026; 0; Mismatches 160; Indels 3153 TAAAA 3157 408 GAACA 412 108 2853 168 228 ઠે 셤 ð 셤 ઠે 요 ð 셤

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proliferative disorder; non methylated CpG dinucleotide; cancer; adenoma; carcinoma; cytosine methylation state; ds
                                                                                                colon cell proliferative disorder;
                                                                           Pretreated genomic DNA region 231
        ADB54307 standard; DNA; 5987 BP
                                                       (first entry)
                                                                                                                                     Unidentified
                                                                                                                cytostatic;
                                                       04-DEC-2003
                                ADB54307;
ADB54307
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The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one geneen colon cell proliferative disorders associated with at least one care reagilatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of reagents, distinguishes between methylated and non methylated CpG dinuclectides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid) coligomers are useful as probes for determining cytosine methylation state or single nucleotide colon of the invention. This sequence is that of the pretreated genomic DNA region of the invention. This sequence is not shown within the specification but is taken from Wipoweb.
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                                                                                                                                                                                                                                                                         Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 GGITAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 49; DB 9; Length 5987; llarity 47.5%; Pred. No. 0.026; Conservative 0; Mismatches 160; Indels
                                                                                                                                                                                    Becker E,
                                                                                                                                                                                    Nimmrich I,
                                                                                                                                                                                                                                                                                                                                                                          Claim 32; SEQ ID NO 363; 74pp; English
                                                                                                                                                                                      Maier S,
                                                                        27-FEB-2003; 2003WO-EP002035.
                                                                                                           27-FEB-2002; 2002EP-00004551.
                                                                                                                                                                                    Adorjan P, Burger M,
Rujan T, Schmitt A;
                                                                                                                                                                                                                                          WPI; 2003-731620/69.
                                                                                                                                               (EPIG-) EPIGENOMICS
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Matches 145; Conserv
                                    04-SEP-2003
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BP. ADB54179 standard; DNA; 5987 RESULT 10 ADB54179 ID ADB5 XX

TAAAA 3157

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GAACA 412

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ADB54179;

The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one between colon cell proliferative disorders associated with at least one care is regulatory regions. The method comprises contexting a target nucleic acid in a biological sample obtained from the subject with at cleast one reagent or a series of reagents, where the reagent or series of reagents distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenda and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide cypolymorphisms. The current sequence is that of the pretreated genomic DNA region of the invention. This sequence is not shown within the specification but is taken from Wipoweb. 2853 Trirririangarirganirgiaririrriranaaaririgiraniriraaagirira 2912 108 TITCIAIICIIGGCCAIIAICIIGIIIICIICGCCGAAIGAICIICCGIAIAAAGAIIIIA 167 228 CTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTCTTATTCGGCGATTGTTGA 287 288 TTAGGGTTTTTGATTTTCTTGATTATTGCAATTAGGGATTTTCTTTGGTTTTGTGT 347 Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with colon cell proliferative disorder, non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ds 348 TGATCTTACGATACATTCCTGCAATTGAATACGTATGGATCTAAATCTTGTTAATTTGTT 168 GGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCT Sequence 5987 BP; 1754 A; 96 C; 1096 G; 3041 T; 0 U; 0 Other; DB 9; Length 5987; Query Match 11.7%; Score 49; DB 9; Length 598 Best Local Similarity 47.5%; Pred. No. 0.026; Matches 145; Conservative 0; Mismatches 160; Indels Nimmrich I, Becker E, Claim 32; SEQ ID NO 235; 74pp; English. Pretreated genomic DNA region 103. Maier S, 27-FEB-2003; 2003WO-EP002035. 27-FEB-2002; 2002EP-00004551. (first entry) (EPIG-) EPIGENOMICS AG Burger M, Schmitt A; WPI; 2003-731620/69 WO2003072821-A2. Unidentified. 04-SEP-2003 Adorjan P, Rujan T, reagent В 음 g à g à 8

The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences of the sequences and their complements The chemical pretreatment is bisulphite tratment to convert cytosines (but not methyl-cytosines) into uracilis. Also included are an oligomer (II) in particular an oligomer one compenies (but not methyl-cytosines) into uracilis. Also included are an oligomer (II) in particular an oligomer one compenies (but not methyl-cytosines) into uracilis. Also included are an oligomer (II) in particular an oligomer one sequence having a length of 9 mucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with complements and their complements associated with the methylation state (CpG) and/or detecting SNPs (single nucleotide polymorphisms) of the 87 squences. The coligomer may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence data for this patent did concerned to the printed specification, but was obtained in continuity and concern the present sequence data for this patent did of the printed specification, but was obtained in continuity and concern the present sequence data for this patent did of the printed specification, but was obtained in continuity and concern the present sequence data for this patent did of the printed specification, but was obtained in the printed specification, but were one the 87 DNA continuity and concern the continuation of the printed specification and concern the continuation of the printed specification and New nucleic acid, oligonuclectides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer. Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11B1; CYP3A3; DFVD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism. Sequence 15479 BP; 4303 A; 122 C; 2850 G; 8204 T; 0 U; 0 Other; Human chemically pretreated gene sequence #23 strand 1. ftp.wipo.int/pub/published\_pct\_sequences Claim 1; SEQ ID NO 45; 24pp; English Berlin K; ABK39964 standard; DNA; 15479 BP. 29-JUN-2001; 2001WO-EP007470 30-JUN-2000; 2000DE-01032529. 21-MAY-2002 (first entry) Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG. WPI; 2002-154757/20. 3153 TAAAA 3157 408 GAACA 412 WO200202806-A2. Homo sapiens. ABK39964; RESULT 11 ò

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Score 48.8; DB 6; Length 15479; Pred. No. 0.034;

11.7%; 51.9%;

Query Match Best Local Similarity

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Gaps ö

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAS45596-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; praft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritis; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
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                              263
                                                                                                                                                   383
                                                                                                                                                                                                                                                                                                                                                                                                       Chemically pretreated complementary DNA associated with cell cycle #14.
                           CTAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGA
                                                                                                                   11317 irriarrarriadaargirrirdairrrrrarrarrarrirrirrrarrarrarrgiderrr
                                                         264 TIGITCITALICGECGALIGITGALIAGGGITITGALTITCITGALTAIGCGALTGCAAI
                                                                                                                                                 324 TAGGGATTTTCTTTTGTGTTGATCTTACGATACATTCCTGCAATTGAATACGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.
   Gaps
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   Indels
    Mismatches 102;
                                                                                                                                                                                                                                           384 GGATCTAAATCTTGTTAATTTGTTGAACAGAT 415
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2000DE-01019058.
2000DE-01019173.
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01-SEP-2000; 2000DE-01043826
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      Conservative
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06-APR-2000; 2
07-APR-2000; 2
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The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                       TATTCGGCGATTGTTGATTTAGGGTTTTTGATTTATGCGATTGCAATTAGGGAT
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                                                                                                                                                                                                     91 AAATTAGGCGAGATTAGTTTCTAGTCCATTATCTTGTTTCTTCGCCGAATGATCT
                                                                                                                                                                                                                                                                                                              1286 İTTITITITICIATİTİAĞAİİTITAĞGGIATGAAİAİATTATTTAİTIAİTGATAĞAAGTİ
                                                                                                                                                                                                                                                                           TCCGTATAAAGATTTTTAGGGTTAGAATGGATGAATAGCTAGATTTTCATCACCAGATAGT
                                                                                           Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T; 0 U; 6 Other;
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                                                                                                                            11.6%; Score 48.4; DB 4; Length 17848; Larity 46.9%; Pred. No. 0.044; Conservative 0; Mismatches 171; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chemically pretreated gene sequence #29 strand 2.
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                     Similarity
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                                                                                                                                                                      Matches 151;
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the Genes AlbH6 (NM 00053), CYP1A (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (NM 000781), CYP1A1 (CYP1A1 (NM 000781), CYP1A1 (CYP1A1 (CYP1A1 (NM 000781), CYP1A1 (CYP1A1 (CYP1A1 (NM 000781), CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1A1 (CYP1
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Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T; 0 U; 6 Other;

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                                                                                                                      1286 TTTTTTTTTTTTAGATTTTAGGGTATGAATATATTATTTATTTATTGATAGAAGTT 1345
                                                                                                                                                                                                                                                                                        1466 TGTTTTTTGATGTTGGTTTTGTTTTTTTTAATTTATGTTTATATTTGTGGTTAGATTGA 1525
                                                                                   91 AAATTAGGCGAGATTAGTTTCTATTCTTGGCCATTATCTTGTTTCTTCGCCGAATGATCT 150
                                                                                                                                                                 TCCGTATAAAGATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGT 210
                                                                                                                                                                                                                                                                                                                             271 TATTCGGCGATTGTTGATTAGGGTTTTGATTTTCTTGATTATGCGATTGCAATTAGGGAT 330
                                                                                                                                                                                                                                              TICITIGICIAGAATCICIGAAATICICGATAGITTTCACATGIGTAAATAGATTGITCT 270
                                                                                                                                                                                                                                                                                                                                                                                                            331 TITCTITGGTTTTTGTGTTGATCTTACGATACATTCCTGCAATTGAATACGTATGGATCTA 390
Score 48.4; DB 6; Length 17848;
Pred. No. 0.044;
0; Mismatches 171; Indels 0;
Query Match
11.6%; Score 48.4;
Best Local Similarity 46.9%; Pred. No. 0.
Matches 151; Conservative 0; Mismatche
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DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNP; retrovital infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; wener syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; erythropoiesis;
                                                                                                                                                                              DNA transcription associated complementary genomic DNA #19.
                                             ABK28164 standard; DNA; 17848 BP
                                                                                                                                   23-APR-2002 (first entry)
                                                                                        ABK28164;
RESULT 14
                          ABK28164
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151 TCCGTATAAAGATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGT 210

91 AAATTAGGCGAGATTAGTTTCTTTGGCCATTATCTTGTTTCTTCGCCGAATGATCT 150

Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T; 0 U; 6 Other;

Query Match 11.6%; Score 48.4; DB 6; Length 17848; Best Local Similarity 46.9%; Pred. No. 0.044; Matches 151; Conservative 0; Mismatches 171; Indels 0;

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271 TATTCGGCGATTGTTGATTAGGGTTTTTGATTTTTCTTGATTATGCGATTGCAATTAGGGAT 330

211 ȚICTȚȚGTCȚAGAAȚCȚCTGAAAȚŢCŢCGATAGTŢŢŢCACATGTGTAAAŢAGATTGTŢCT 270

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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligomicleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cranscription. The set of oligomer probes are useful for detecting the cranscription. The set of oligomer probes are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, hemmal-plot disorders, immunological disorders, warner syndrome, thermological disorders, immunological disorders, syndrome, conserving syndrome, arthritis, polyglutamine disorders, myocardial infarction, hypertension, angiogenesis, erythropolesis, congenital heart disorders associated genomic DNA molecules of the invention. Note: The sequence of associated genomic DNA molecules of the invention. Note: The sequence dates for this parent did not form part of the printed specification but was obtained in electronic format directly from the European Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumors or
myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
                angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 38; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin K;
                                                                                                                                                                                                                                                           06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UUN-2000; 2000DE-01035529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                     06-APR-2001; 2001WO-EP003973
                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-090046/12.
                                                                                                                             WO200192565-A2.
                                                                                   Unidentified.
                                                                                                                                                                          06-DEC-2001.
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us-09-000-062-6.rng

Seguence 2501 BP; 532 A; 124 C; 707 G; 1138 T; 0 U; 0 Other;

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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least I gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with a least 1 reagent, which distinguishes between methylated and non-methylated CDC dinuclectides within the target nucleic acid. AEZ09861 to AEZ1118 represent specifically claimed nuclectide sequences from the present invention. Oligonuclectides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells and proliferative disorder haematopoietic cells and proliferative clamphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphiams (SMPS) of haematopoietic cell proliferation disorder related the cytosine methylation state and/or single nucleotide polymorphiams (SMPS) of haematopoietic cell proliferation disorder related the cytosine methylation state and/or single nucleotide polymorphiams (SMPS) of haematopoietic sell proliferation disorder related the cytosine methylation state and/or single nucleotide polymorphiam (SMPS) of haematopoietic cells and successive contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and the cytosine methylation state and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contactions and contacti
                                                                                                                1466 TGTTTTTTTGATGTTGGTTTTGTTTTTTTAATTTTAAGTTTATATGTGGGTTAGATTGA 1525
Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                    331 TITCITIGGITITGIGITGATCITACGATACATICCIGCAATIGAATACGTATGGATCTA 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haematopoietic cell proliferation disorder related DNA sequence #214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia, cytosine methylation state; gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
Lewin A, Lipscher E, Maier S, Model F, Mueller V, Otto T, I
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 28; SEQ ID NO 214; 117pp; English.
                                                                                                                                                                                                                             1526 ATATGAATAATATTGTTATA 1547
                                                                                                                                                                     391 AATCTTGTTAATTTGTTGAACA 412
                                                                                                                                                                                                                                                                                                                                                                         ABZ10074 standard; DNA; 2501 BP
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1661 TITATATITITIGAGAITITAGITITGGGITTAAATAGITITGAITITAAATIGITGAAGGGA 1720
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                                                                                                                                                                                                                                                                                                                                                 205 GATAGTTTCTTTGTCTAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGAT 264
                                                                                       25 TTGATTTTCCTGGAAATATTTTTCGGTGATCGTGAAACTACTGGAATCGCTCGATAGGT 84
                                                                                                                                                                           85 GGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGGCCATTATCTTGTTTCTTCGCCGAA
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11.5%; Score 48; DB 7; Length 2501; 47.1%; Pred. No. 0.04; tive 0; Mismatches 200; Indels
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related sequences and their complements, and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The muclecides sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of memarcopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients

Title:

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AL950952 Arabidops BX43359 BX435369 BX436369 AL555108 AL555108 AL556108 AL5010000 AL1000000 Drosophil AL0524607 AL052407 AL052205 Drosophil AL052407 AL09126 Drosophil AL10531 Drosophil AL10593 Drosophil AL10593 Drosophil BX43528 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX31505 BX33350 BX33350 BX33350 BX40550 BX3350 BX40550 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX4050 BX333369 BX333369 BX333369 BX333369 BX333369 BX437039 BX333369 BX437039 BX437039
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                                                                                                     BX331505
CNS01090
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BX399782
BX462904
CNS07ABZ
BX462904
CNS00519
CNS006N9
CNS006N9
CNS006N9
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   BH633573
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BH633573/c
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Result

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                                                                                            /organism="Arabidopsis thaliana"
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome Unpublished (2001)
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Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 366)
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                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGAAATATTTTTCGGTGATCGTGAAACTACTGGAATCGCTCGATAGGTGGTACGAA
   This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of At4g40040. Class: TDNA tagged.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           DB 28; Length 436;
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Pred. No. 1.6e-67;
0; Mismatches 2; Indels
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llarity 99.5%;
Conservative
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Best Local Si
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/mol_type="genomic DNA"
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Arabidopsis thaliana T-DNA flanking sequence GK-329E10-016035, genomic survey sequence.
AL950572
AL950572.1 GI:24407194
GSS.
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Arabidopsis thaliana
Brakaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border this is single pass sequence lies within 300 bases of the 5' end of Ar4940040.
Class: TDNA tagged.
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genomic survey sequence.
Arabidopsis thaliana
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nes 193; Conserv
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Direct Submission

Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-OCT-2002) Weisshaar B., Max-Planck-Institut fuer
Indicates an insertion close to or within gene Ar4940040. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:3702"
/clone="GK-329E;0-016035"
/clone="GK-329E;0-016035"
/clone="Taxobioopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pActifi. The lines contain one or more T-DNA from were directly sequenced to determine the genomic sequence flanking the insertion. Sequenced to determine the genomic sequence similarity to the A. thalaina nuclear genome sequence similarity to the A. thalaina nuclear genome sequence processed for submission. T-DNA derived sequences were
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Arabidopsis thaliana T-DNA flanking sequence GK-329E10-016044,
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                                                                                                                                                                       Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B.
A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat)
for flanking sequence tag based reverse genetics
             Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 TAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTCTTATTCGGCG
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                                           A pipeline for automated high-throughput generation of Fi
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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llarity 99.5%; Pred. No. 8.4e-30;
Conservative 0; Mismatches 1;
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Matches 195; Conserv
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Submitted (21-07T-2002) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion close to owthin gene At4940040. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:

Location/Qualifiers
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Arabidopsis thaliana T-DNA flanking sequence GK-332E10-016059,
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                                                                                                      Dekker, K., Saedler, H.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermarophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                 A pipeline for automated high-throughput generation of FG
(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                   Strizhov,N., Li,Y., Rosso,M. and Weisshaar,B.
Direct Submission
                                                                                                    Strizhov, N., Li, Y., Rosso, M., Viehoever, P., and Weisshaar, B.
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AL565108/c
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BX436369 BX436369-1 GI:30787529
                                                                                                                                                                                                                                                                                                                                                                                                                              July Y., Strizhov, W., Rosso, M. and Weisshaar, B.

Direct Submission

Submitted (21-0cT-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (21-0cT-2002) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion close to or within gene Ar4940040. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgq.de/GABI-Kat/.
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. Inalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
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                                                        Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                       Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                             Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
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/clone="GK-332B10-016059"
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                        GI:24407574
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/tissue_type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: PCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, cobble-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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ALS65108 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
CSODN004YK09 3-PRIME, mRNA sequence.
ALS65108
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1180)
1 (Jam. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSOCAP001BG06QP1&cluster=516.f. Contact
cgi-bin/cluster.cgi?seq=cSOCAP001BG06QP1&cluster=516.f. Contact
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP001BG06QP1.
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                                                                                                                                                                                                                                Contact: Genoscope
Genoscope - Centre National de Sequencage
BPP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 516.f
more information about this cluster, see
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.larity 27.3%; Pred. No. 0.067;
Conservative 101; Mismatches 195; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP001YM12"
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AL524807 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens ODNA CLONA CLONE CSODC008YK01 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                            Genoscope.

Direct Submission

By 191 91006 ENRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence was carried out as part of a trtp://www.edgp.ebi.ac.uk - This Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       530 iCarrrirrirrirrirrirrirccrrrrrrrarkkiwrrkrrrrrrrwrrwgkrr 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 TCGCTCGATAGGTGGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGGCCATTATCTTG
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebyydroidea; Drosophilidae; Drosophila.
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32.1%; Pred. No. 0.2;
ive 74; Mismatches 195;
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/mol type="genomic DNA"
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1. .750
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Matches 127; Conservative
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KEYWORDS
SOURCE
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JOURNAL
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AL100303
AL100303.1 GI:5611914
GSS.
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[1 (Dases 1 to 1180)
[2 [1./ W. B., Gruber, C., Jessee, J. and Polayes, D.
[3 [1./ W. B., Gruber, C., Jessee, J. and Polayes, D.
[4 [1./ W. B., Gruber, C.]
[5 [1./ W. B., Gruber, C.]
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/clone_lib="Homo sault"
/clone_lib="Homo sault"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."
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/db_xref="taxon:9606"
/clone="CSODN004YK09"
                             GI:31289080
                                                                                                   sapiens (human)
                                                                                                                                                     sapiens
                                                                                                                    Ношо
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Gaps

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Length 750; Indels 411

351 251 ø

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Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                      Genoscope
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CNS0081L/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 i.W.B.; Gruber,C.; Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Lungublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12788300.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3928.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODO008AFOINPL&Cluster=3928.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODCO08AFOINPL.
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AL059925 AL059925.1 GI:4943047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue type="MEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector Library was normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (fruit fly)
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC008YK01"
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Direct Submission

Submitted (102-UNN-1999) Genoscope - Centre National de Sequencage :

By 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Constructed by partial Cancer Genetics at the Roswell Park Cancer Constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pland how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brosophila melanogaster genome survey sequence TET3 end of BAC #BACR16N08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 GTAAATAGATTGTTCTTATTCGGCGATTGTTGATTAGGGTTTTTGATTTTCTTGATTATGC
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 960)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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Best Local Similarity 40.29
Matches 158; Conservative
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us-09-000-062-6.rst

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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// organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/db xref="texon:966"

/clone="CSODA011V114"

/tissue_type="NEUROBLASTOMA"

/tissue_type="NEUROBLASTOMA"

/tissue_type="NEUROBLASTOMA"

/tissue_type="NEUROBLASTOMA"

/note="Wector: PCMVSPORT 6; lst strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, with a Not1-oligo(dT) primer. Five prime end enriched, with a Not1 and scoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 TITAGGITAGAGIGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 ATCTCTGAAATTCTCGATAGTTTTCACATGTGAAATAGATTGTTCTTATTCGGCGATTG
                                                                           Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Paraday Avenue Genoscope sequence ID : CSODA011BE07QP1.
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebyydroidea; Drosophilidae; Drosophila.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL097301.1 GI:5608912
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Submitted (02-UNW-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

The Bot sww.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Rowell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecopi and for Drosophila DNA provided by the BDGP from the isogenic strain v2: or by, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Quallifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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/mol_type="genomic DNA"
/db_xref="reaxon:7227"
/clone="BACR16N08"
/clone lib="RPCI-98"
/note="end : TET3"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACL BACL BACL BACL SILDER FOR DROSOPHILA melanogaster (fruit
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            Use : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre Stands et W Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                melanogaster"
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/ organism="Drosophila mel,

/ mol_type="genomic DNA"

/ db_xref="texon:727"

/ clone="BACNO1A10"

/ clone libe"DrosBAC"

/ plasmid="pelosAc11"

/ note="end : T7"
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larity 33.0%;
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CNSO14RT 975 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN12L12 of DrosBAC library from Drosophila melanogaster (fruit
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Submitted (23-UTL-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
1 (bases 1 to 975)
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Pred. No. 1.4;
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Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                              /mol type="genomic DNA"
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/clone="BACN18B.6"
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/note="end : T?"

    .894
    organism="Drosophila"

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AL104531
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us-09-000-062-6.rst

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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.adgp.ebi.ac.uk -. This Drosophila melanogaeter BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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1. 975
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Job time : 2075.67 secs
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Arabidopsis thallana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; endicotyledons; core eudicots;
Spermatophyta; Magnollophyta; endicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 300)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL.http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
AV551146 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cobh clone RZ121h02R 5', mRNA sequence.
AV551146 GI:8722559
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CNS0012B
BU534806
CG7441146
CG7444146
CNS0011D
CG749401
CG7749401
CG7749401
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CG7749401
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Z34742 ATTS3502 St
BX416727 BX416727
AL101645 Drosophil
                                                                                       June 20, 2004, 01:39:08; Search time 2448.33 Seconds (without alignments) 6025.290 Million cell updates/sec
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(c) 1993 - 2004 Compugen Ltd.
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14 Z34742
13 BX416727
29 CNS012JN
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Maximum DB seq length: 2000000000
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Query Match
Best Local Similarity 85.3%;
Matches 273; Conservative
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Arabidopsis thaliana
Buaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 320)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone lib="Strasbourg-A"
/note="Vector: Lambda ZAPII; tissue=sliced leaves of
A.thaliana ecotype columbia; clone library=Strasbourg-A;
Cloning vector: Lambda ZAPII; Physiological condition:
leaves strips incubated 2/3/4 days in liquid culture
medium."
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                                                                                                                                                                                                                                                                                                                                                                                                                                              212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Arabidopsis thaliana transcribed genome: the GDR cDNA program Unpublished (1996)
Contact: Philipps G., Gigot C.
Gigot Claude / L512
Laboratoire de Biologie Moleculaire des Plantes - CNRS
12 Rue du General Zimmer, 67084 Strasbourg Cedex, France
Email: ARABANKGMEDOC.1-STRABG.FR.
Location/Qualifiers
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
factotype Columbia"
/db xref="texcn:3702"
/clone="FAI185"
1. .300
/organism="Arabidopsis thaliana"
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BX416727 Thomo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CSODA011Y114 5-PRIME, mRNA sequence.
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1 (bases 1 to 712)
1 (bases 1 to 712)
1 (Auber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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/tissue type="NETROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned ithe Not I and cooky sites of the pCMVSPORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                               121 TTCCAAGTTTGAAAATAAAGGTCCCGTCTTTTAAGTTTGCTGGATCGATAAACCTGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégencoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : filangelifetech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA011BE07QP1.
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Score 202.8; DB 14; Length 320;
Pred. No. 5.5e-32;
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larity 13.4%; Pred. No. 0.0058;
Conservative 179; Mismatches 165;
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Homo sapiens
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ALIO1645.1 GI:5613256
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila denome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CBPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                  486
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                                                                                                                    129 GICCCAITCCAGTITGAAATAAACGICCGICTTITAAGTITGCIGGATCGATAAACCTG 188
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                                                                                       249 CGAAGTICTGTATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCGTGTATCGA
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebyydroidea; Drosophilidae; Drosophila.
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ilarity 40.9%; Pred. No. 0.14;
Conservative 36; Mismatches 203;
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Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage:
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.

1. icoation/Qualifiers
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AL228940.
AL228940.1 GI:7887933
GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
Tetraccan proviridis
Actinopterygii, Neopterygii, Teleostei; Euteleostei;
Actinopterygii, Acanthopterygii; Percomorpha; Tetraccontiformes;
Tetraccontoidea; Tetraccontidea; Tetraccontiformes;
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Terraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                          TACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTTCGGGTTTTGTCCCATTCCAGTT
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Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I 10 131)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

CDNA Library Preparation: Gina Zastrow-Hayes

CDNA Library Preparation: Gina Zastrow-Hayes

CDNA Library Arrayed Dy: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDKM32 row: m column: 05

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High quality sequence story: 257.
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/clone="214A06"
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/note="Genoscope sequence ID : COAG214BA03SP1-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       378 AGGGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCTTCAAAATTTAGTTAT 429
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                                                                                                                                            10.9%; Score 54; DB 29; Length 576; 40.8%; Pred. No. 0.21; cive 27; Mismatches 217; Indels
organism="Tetraodon nigroviridis"
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/mol_type="mRNA"
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                                                                                                                                                                              Conservative
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                                                                                                                                                                Similarity
                                                                                                                                                                                168;
                                                                                                                                               Query Match
Best Local S:
Matches 168
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/tissue_type="embryonic trophoblasts, made from WA01 stem
cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA linear GSS 26-JUL-15
DNOSOPhila melanogaster genome survey sequence T7 end of BAC
BACNO1602 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                           /clome_lib="NIH_MGC_173"
/note="Vector: pDONR201; Site_1: attP2; Site_2: attP1;
LIBR_PRIMING - oligo dT; METHÖD - full-length enriched;
LIBR_PROVIDER - Bzadfield"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 TACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCCATTCCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TGAAAATAAACGTCCGTCTTTTAAGTTTGCTGGATCGATAAACCTGTGAAGATTGAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 GAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCATCTGGATTAGGGT
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Drosophila melanogaster
Bukaryota, Metazoa; Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                               Length 1131;
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                                                                                                                                                                                                                                                                           10.6%; Score 52.4; DB 14;
llarity 45.4%; Pred. No. 0.37;
Conservative 0; Mismatches 226;
                                                                 host="DH10B TonA
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                                                                 /lab
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pBeloBAC11.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN13P09 of DrosBAC library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Bucopean Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - This Drosophila Genome Project (BDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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                                                                                                                                                                                                                                                                                             426
                                                                                                                                                                                                                                                                                                                                     TCTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCCATTC 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       258 GIAȚAACCAGATȚTGICIGTGIGCGAȚTGICAȚTACCIAGCCGIGTATCGAGAACTAGGG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITICGAGICAATITIGCCCCTITIGGTTATATCTGGTTCGATAACGATTCATCTGGATT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 AGGGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCAAAATTTAGTTATGGATAATG 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterydota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                            DB 29; Length 683;
                                                                                                                                                                                                                    Indels
/organism="Drosophila melanogaster"

/mol 'type="genomic DNA"

/db xref="raxon:7227"

/clone="BACNO1G02"

/clone lib="DrosBAC"

/plasmid="BpelcBAC11"

/note="end : T7"
                                                                                                                                                                            10.5%; Score 51.8; DB 29;
llarity 33.5%; Pred. No. 0.56;
Conservative 5; Mismatches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  438 AAAATCCCGAATTGACTGTTCAATTTCTTGTTAA 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 NTAWITNIAAIAIINIITAAIITIIIITA 32
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                                                                                                                                                                                Query Match
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 813)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (199)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95 TÖGCWITTWWITACITTTWTTWTTTTWWWWITWTTWTTWTTTTWAATTCATAATTTGCW 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 GATCCATTCTTCATCGTTTTTTTTTTGTTGAAGTTCTGTATAACCAGATTTGTCTGTG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 TGCGATTGTCATTACCTAGCCGTGTATCGAGAACTAGGGTTTTCGAGTCAATTTTGCCCC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      399 TAGTATICCAATITCTICAAAATITAGTTATGGATAATGAAAATCCCGAATTGACTGTTC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335 TKTTAYTWTTTTTTTTTTTTTTTTTTTTTGGTTACAWTTWAAWWTYTACCGGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 iriririruwiririkirwiddikarwwiwrruririririririririririririi 334
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Tissue Produzement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloseience Corporation
Clone distribution: MG Clone distribution information can distribution: MG Clone distribution information can http://image.llnl.gov
Plate: LCMA737 row: 1 column: 02
High quality sequence stop: 141.
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AGENCOURT 10183661 NIH_MGC_143 Mus musculus cDNA clone IMAGE:6562130 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                       Length 942;
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                                         melanogaster"
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10.5%; Score 51.8; DB 29;
Best Local Similarity 36.3%; Pred. No. 0.51;
Matches 113; Conservative 48; Mismatches 150;
1. .942

/organism="Drosophila mel.

/mol_type="genomic DNA"

/db_xref="texon:7227"

/clone="bACN13F09"

/clone="bBCN13F09"

/plasmid="pBeloBAC11"

/note="end:17"
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/db_xref="taxon:10090"
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22835951
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/mol type="genomic DNA"
/strāin="California"
                                                                                                                                                                                                                                                                                                                       10.4%; Score 51.2; DB 29;
llarity 33.2%; Pred. No. 0.72;
Conservative 62; Mismatches 165;
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Max-Planck-Institute for Developmental
Spemannstr. 37-39, Tuebingen D-72076, G
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
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Pristionchus pacificus
Eukaryota, Metazoa, Chr
Neodiplogasteridae, Pristionchus.
                                                       /organism="Drosophila me/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN06D21"
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/note="end : T7"
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                        /lab_host="DH10B (T1.phage-resistant)"
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN06D21 of DrosBAC library from Drosophila melanogaster (fruit
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Submitted (23.-UU.-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Get : www.genoscope.cns.fr - Get : www.genoscope.cns.fr - Get : www.genoscope.cns.fr - Get : www.genoscope.cns.fr - This BAC-end sequence was carried out as part of a collaboration with the European Droscophila Genome Project (EDGP) - http://www.edgp.eb/i.ac.uk - This Droscophila melanogaster BAC - Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Larity 32.3%; Pred. No. 0.63;
Conservative 0; Mismatches 235; Indels 0
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Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., An integrated physical and genetic map of the nematode Pristionchus Politicus.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR16L07 of RPCI-98 library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was propared by Kazutoy oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 741)
/db_xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
the genomic DNA with EcoRI and cloning into the BAC
vector."
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Pred. No. 0.69;
0; Mismatches 275; Indels
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563 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TBT3 end of BAC #BACR16P14 of RPCI-98 library from Drosophila melanogaster (fruit Fly), genomic survey sequence.
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Direct Submission
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Small Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
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BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's P1 and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                              Length 741;
                                                                                                                                                                                                                                                                                                                                            Score 50, DB 29, Length 74
Pred. No. 1.3;
0, Mismatches 293; Indels
                                                                                                                                                                            /organism="Drosophila melanogaster"
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/clone="BACR16LO7"
/clone lib="RPCI-98"
/note="end : TET3"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on was, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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ALO51476
ALO51476.1 GI:4933530
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 737)
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/note="end : TET3"
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- Web : www.genoscope.cns.France (B-Mmill : Begrelegenoscope.cns.II.

Determination of this BAC-end sequence was carried out as part of collaboration with the Barkeley Drosophila genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see thtp://www.fruiffly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library, and how to order individual BAC clones, the entire library, or filters for hybridization from the BACFAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Pristionchus pacificus
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Best Local Similarity 33.34
Matches 138; Conservative
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 1403)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., An integrated physical and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
Mol. Genet. Genomics 269 (5), 715-722 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1403

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/strain="California"

/db_xref="taxon:54126"

/clone_lib="Ppa EcoRI BAC Library"

/note="The library was generated by a partial digest of

the genomic DNA with EcoRI and cloning into the BAC

vector."
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Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
Location/Qualifiers
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## ALIGNMENTS

Arabidopsis thaliana histone H3.3-like DNA fragment (intron 2) AAT85997 standard; DNA; 494

Plant expression regulation sequence; intron 2; histone; herbicide tolerance; 5-enolpyruvylshikimate-3-phosphate synthase;

96WO-FR001109

Gigot C;

New regulatory sequence for chimeric gene expression in rapidly growing parts of a plant - includes at least one intron from a plant histone gene and is useful for imparting resistance to herbicides.

The known cosmid clone c22 of Arabidopsis thaliana contains two histone H3.3-like genes. Digestion of clone c22 with restriction enzymes Alul and Cfol generated a fragment of 494 bp having the present sequence. This fragment, designated intron 2, was ligated to synthetic linkers for cloning into plant expression vectors. In addition to the intron 2 sequence, the vectors contained a plant promoter and a herbicide tolerance gene (e.g. a mutated version of the 5-enolpyruvylshikimate-3-phosphate synthase (BPSPS) gene). The intron enhances expression of the herbicide tolerance gene in rapidly growing parts of plants. The intron can also be used to enhance expression of genes that impart resistance to

us-09-000-062-7.rng

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pathogens or that encode nutritional or therapeutic proteins
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated With pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 000693), CYP11A (NM 000781), CYP11B (NM 000797), CYP1A (NM 000781), CYP11B (NM 000781), CYP11B (NM 000518), CYP1A (NM 000781), CYP1A (NM 000797), CYP1A (NM 000797), CYP1A (NM 000797), CYP1A (NM 000797), CYP1A (NM 000776 and NM 019901, NM 019802) NM 019802) NM 019802) NM 019802, NM 019809) and their complementary sequences, or a sequence (S1) chosen From 87 careament to convert cytosines (NM 019908, NM 019909) into utacils. Also included are an oligomer (II) in particular an oligometical action or a peptide nucleic acid (NNA)-oligomer, comprising in each case at least one peptide nucleic acid (NNA)-oligomer, comprising in each case at least one peptide nucleic acid (NNA)-oligomer, comprising in each case at least one compared to a chemically pretreated DNA of genes associated with the methylation state (CpS) and/or detecting SNPS (single nucleotide polymorphisms) of the 87 sequences. The cligomers may also be used as PCR primers. The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence data for this patent did concern form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid, oligonuclectides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.
               Human, ds, bisulphite treatment, CpG, DNA methylation; cancer; tumour; cytostatic, ALDH6; CYP11A; CYP11B1; CYP3A3; DPYD; EPHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
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2000DE-01043826.
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The invention relates to a nucleic acid comprising a sequence of at least with call signaling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as objectnicerides and/or PNA-oligomers for provide the chemically modified DNA of genes associated with cell signalling, as well as objectnicerides and/or PNA-oligomers for particularly suitable for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as sociated with cell signalling. The signal in records ABL70111-ABL70626 represent chemically pre-treated given in records ABL70111-ABL70626 represent chemically pre-treated sequence data for this patent is not represented in the printed sequence data for this patent is not represented in the printed sequence and provided by the confidence information supplied by the ö 3327 ITTIAGITTITATITGITTTTTATTTTTTTTTATTTAAAITTTTATTTTTTAGGAAGITTT 3386 Cell signalling, cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds. Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling. 258 GTATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCGTGTATCGAGAACTAGGG 318 TTTTCGAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCATCTGGATT Gaps Sequence 12870 BP; 3115 A; 234 C; 3273 G; 6248 T; 0 U; 0 Other; ö 11.3%; Score 55.8; DB 6; Length 12870; ilarity 46.5%; Pred. No. 0.0002; Conservative 0; Mismatches 207; Indels 0; Claim 1; SEQ ID NO 119; 24pp + Sequence Listing; English. Chemically treated cell signalling DNA sequence#60. 3507 radaagiicgdiadddracaiadiri 3533 378 AGGGTTTTAAGTGGTGACGTTTAGTAT 404 Ϋ́ ם Berlin ABL70229 standard; DNA; 12870 29-JUN-2001; 2001WO-EP007471. 30-JUN-2000; 2000DE-01032529. (first entry) Piepenbrock C, (EPIG-) EPIGENOMICS AG. European Patent Office Query Match Best Local Similarity Matches 180; Conserva WPI; 2002-154758/20 WO200202807-A2. Unidentified 01-JUL-2002 10-JAN-2002 ABL70229; olek A, g à g à 유 ò

their complementary sequences, or a sequence (S1) chosen From 87 sequences and their complements. The chemical pretraetment Es bisulphite treatment to convert cytosines (The chemical pretraetment is bisulphite treatment to convert cytosines (Dut not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligomucleotide or a peptide nucleic acid (PNA) oligomer. (Comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with pharmacogenomics and their complements, arranged in an array for detecting SNPs (single nucleotide polymorphisms) of the 87 sequences. The caligomers may also be used as PCR primers. The set of 87 nucleic acids on their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence represents one the 87 DNA sequences or its complement. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MPO at

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                                                                                                          3447 Tragrgaaracgraridararririranaaraarriradigerrrriggrirririrririr 3506
                                                             3207 TATAGTITITAATATAGTITIGITITITITATIGGTITITAGATAIGITITGTICGTITT 3266
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                                                                                     CAGITIGAAAATAAACGICCGICITITIAAGITITGCIGGAICGAIAAACCIGIGAAGAITG
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TATGATTTGTAATTAGATCAGGGGTTTAGGTCTTTCCATTACTTTTAATGTTTTT
                     Human chemically pretreated gene sequence #1 strand 2.
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                                                                                                                                                                                                                                                                            Sequence 17869 BP; 5366 A; 158 C; 3365 G; 8978 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                          DB 6; Length 17869;
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46.0%; Pred. No. 0.012;
tive 0; Mismatches 240; Indels
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Matches 210; Conservative
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The invention relates to a nucleic acid comprising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the genes ALDH6 (NM 000693), CYP1A (NM 000781), CYP11B (NM 000776 and NM 017460), DPYD (NM 000110), EPHX2 (NM 01979), OCLN (NM\_002538), TXXRD1 (NM\_003330), UGT8 (NM\_003360), MRP\_(NM\_004996,

New nucleic acid, oligonuclectides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer.

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Berlin

Piepenbrock C,

Olek A,

WPI; 2002-154757/20.

Claim 1; SEQ ID NO 2; 24pp; English

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ABL32478 standard; DNA; 6593

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid thetaemia, Alzhaelmer's disease, Alzhaeliepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197
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                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 AGGGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCTTCAAAATTTAGTTATGGATAATG
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Pred. No. 0.012;
0; Mismatches 240; Indels
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                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                     30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
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Best Local Similarity 46.0%;
Matches 210; Conservative
                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
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                                                                                                            WO200200928-A2.
                                                                           sapiens
                                                                                                                                                                                                                                          01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                  methylation
                                                                                                                                                  03-JAN-2002
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                                                                                                                        antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; ey ey elimentialismmatory; anneemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                       cytosine methylation; antiasthmatic;
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                                                                           Human immune system associated gene SEQ ID NO: 451.
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Pred. No. 0.018;
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                                                                                                           system disease;
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01-SEP-2000; 2000DE-01043826.
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ilarity 45.8%;
Conservative
                                              (first entry)
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Best Local Similarity
Matches 207; Conserv
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Best Local 9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid origoner (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CPG dinucleotides e.g. cancers and tumours. The propession to be used in a method for ascertaining genetic and/or diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
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                                                                                                                         437
                                                                                                                                                 693
 513
                                                573
                                                                                                 633
                                                                                                                                                                                                                                                                                                                                                           Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; cpd dinuclectide; single-nuclectide polymorphism; SNP; cytosine methylation; ds.
514 TİAİGATGAATİTİTİAİTİTAĞTTAİTİĞİATİTTTİATTTTAĞAAİTTTTAİTTİĞTT
                                                                                                                           AGGGTTTTAAGTGGTGACGTTTAGTATTCCCAATTTCTTCAAAATTTAGGTTATGGATAATG
                                                                                                                                                634 ATTTİGİTTAĞİTĞİTTATİTĞĞĞİTİİTTGİAATİTĞTTĞAĞİTATİTAAĞATĞAİT
                          GTATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCGTGTATCGAGAACTAGGG
                                                                        TTTTCGAGTCAATTTTGCCCCTTTTTGGTTATTCTGGTTCGATAACGATTCATCTGGATT
                                                                                                 Tumour suppressor gene derived chemically modified sequence #252
                                                                                                                                                                             469
                                                                                                                                                                                                  694 ATTTTGAATTTTTTGTTAGATAATTTATAGAT 725
                                                                                                                                                                          438 AAAATCCCGAATTGACTGTTCAATTTCTTGTT
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07-APR-2000; 2000DE-01019173.
30-UTM-2000; 2000DE-01052559.
01-SEP-2000; 2000DE-01043826.
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acure myeloid leukaemia; Albrieimer's disease; AlDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumber sequence is one of the 533 genomic sequences and numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and IDI, ID 536 and ID 535, accept for those whose partner sequence is missing). Note: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 GITIGAAATAAAGTCCGTCTTTTAAGTTGCTGGATCGATAAACCTGTGAAGATTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7814 BP; 1677 A; 101 C; 1779 G; 4257 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7814;
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46.8%; Pred. No. 0.043;
tive 0; Mismatches 239; Indels
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(first entry)

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Homo sapiens
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                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                     142
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                                                                                                                                                fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3718 idaratrizaagargrizirgizagizaaraaarrgrizarrarrarrarrarrarra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                323 GAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCATCTGGATTAGGGT
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                                                                                                                                                                                                                                                                                                                                                                                        23 TITGITIGIAATTAGAICAGGGTTTAGGICTTICCATTACTTTTAATGTTTTTCTGT
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0
                                                                                                                                                                                                                                                                                                                       Sequence 6650 BP; 1628 A; 159 C; 1561 G; 3302 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                          9.4%; Score 46.4; DB 6; Length 6650;
4.0%; Pred. No. 0.047;
ive 0; Mismatches 251; Indels 0;
                                                                                                                                                                                              Claim 1; SEQ ID NO 611; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTIGGITGATITGITGAATTITITIA 4045
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                                                                                                      Berlin K;
                                               2000DE-01032529.
2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                         Local Similarity 44.0%;
les 197; Conservative
                          02-JUL-2001; 2001WO-EP007537
                                                                                                                                                   Nucleic acid comprising diagnosis and treatment
                                                                                                        Piepenbrock C,
                                                                                  (EPIG-) EPIGENOMICS AG
                                                                                                                               WPI; 2002-130909/17
                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                           methylation.
    03-JAN-2002
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ID ABL32
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AC ABL32
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Matches
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standard; DNA; 6048

ABL32509 ABL32509

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheimer's disease, Alzheimer's disease, and inflammatorid varthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TIAAGTITGCTGGATCGATAAACCTGTGAAGATTGAGTCTAGTCGATTTATTGGATGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 CATTCTTCATCGTTTTTTTTTTTTCGAAGTTCTGTATAACCAGATTTGTCTGTGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343 GGTTATATCTGGTTCGATAACGATTCATCTGGATTAAGGGTTTTAAGTGGTGACGTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 ATTGICATTACCTAGCCGTGTATCGAGAACTAGGGITTTCGAGTCAATTTTGCCCCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antinframatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzhaimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                      cytosine methylation; antiasthmatic;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 6048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                claim 1; SEQ ID NO 482; 32pp + Sequence Listing; German.
Human immune system associated gene SEQ ID NO: 482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 163;
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                                                             disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-2000;
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2625 TTTTTT 2631

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Haematopoietic cell proliferation disorder related DNA sequence #329.
                                                                Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                    Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Libscher E, Maier S,
                                                                                                                                                        26-MAR-2001; 2001US-0278333P.
            ABZ10189 standard; DNA; 3025
                                                                                                                                           26-MAR-2002; 2002WO-EP003401
                                        (first entry)
                                                                                                                                                                                                   Lipscher E, N
Ziebarth H;
                                                                                                                                                                      (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                       WPI; 2003-018942/01.
                                                                                                                WO200277272-A2.
                                                                                                  Homo sapiens
                                                                                                                                                                                             Olek A, Pie
Lewin A, Li
Schwope I,
                                         16-JAN-2003
                                                                                                                              03-OCT-2002
                           ABZ10189;
RESULT 13
       ABZ10189
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Pelet C;

Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T, I

Guetig D, 1 P, Grabs ( Model F, h

The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ13861 to ABZ1118 crepresent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative cliscorder haematopoietic cells; for differentiating between acute cliscorder haematopoietic cells; for differentiating between acute of sequences and acute myelogenous leukaemia; as probes for celated sequences and their complements; and as primers for the related sequences and their complements; and as primers for the created be used for detecting a predisposition to, differentiation between complements and sequences from the present invention can also be used for detecting a predisposition to, differentiation between cubclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative coll proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The patients Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides. Claim 28; SEQ ID NO 329; 117pp; English

Sequence 3025 BP; 535 A; 0 C; 930 G; 1560 T; 0 U; 0 Other;

ï 82 23 TTTGTTTTTTAATTAGATCAGGGGTTTAGGTCTTTCCATTACTTTTAATGTTTTTTCTGT Query Match
Best Local Similarity 47.9%; Pred. No. 0.049;
Matches 162; Conservative 0; Mismatches 175; Indels

2001 irrakiriakagrirrirakiririkaririraka irringedegiringedegiredege 2059 2120 GGAAGAGIGIGGIGGIGTIGAGITIAGAITGTITAGIAITGIGAGIGIAITITIA 2179 1881 TTGTTTTGGTTTTTAGTGATGTTTTTATTTTTATTATATATGTTTATGTTTTGGGA 1940 263 ACCAGATTIGICIGIGIGGGATTGICATTACCTAGCCGTGIATCGAGAACTAGGGTTTIC 322 дŝ. 203 AGICGATITAȚIGGAȚGAȚCCAȚICȚICAȚCGTTȚTTȚTTTCTȚGCTȚCGAAGTTCTGTAȚA 83 TACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCCATTCCAGTT TGAAAATAAACGTCCGTCTTTTAAGTTTGCTGGATCGATAAACCTGTGAAGATTGAGTCT colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state; ď Lesche Nimmrich I, Becker E, 2180 rrdagadriridregreirideriririridrinderedai 2217 323 GAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGAT 360 Pretreated genomic DNA region 143. Maier S, 27-FEB-2002; 2002EP-00004551. 27-FEB-2003; 2003WO-EP002035. ADB54219 standard; DNA; 3025 (first entry) (EPIG-) EPIGENOMICS AG Schmitt A; WPI; 2003-731620/69. WO2003072821-A2. 04-DEC-2003 04-SEP-2003. Adorjan P, Rujan T, S 143 ADB54219; RESULT 14 ADB54219 g 8 임 ò g ò a à ò

Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject with

Claim 32; SEQ ID NO 275; 74pp; English.

The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contracting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or ascries of reagents, where the reagent or series of reagents, where the reagent or series of includence that the nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative for disorders, including cancers such as colon adenome and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide propagatory. The current sequence is that of the pretreated genomic DNA

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2000
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                                                                                                                                                                                                                                                                                     2059
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                                                                                                                                                               1881 irgriritectritrariraksareitrrraririrariraraharerraheterrahes
                                                                                                                                                                                            83 TACTGICICCGCGAICTGATTTTACGACAATAGAGTTTTCGGGTTTTGTCCAGTT
                                                                                                                                                                                                                                                                                   TGAAAATAAACGTCCGTCTTTTAAGTTTGCTGGATCGATAAACCTGTGAAGATTGAGTCT
                                                                                                                                                                                                                                                                                                                   TICTIGCTICGAAGTICTGTAIA
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                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lymphoid cell proliferative disorder gene derived DNA #93.
                                                                                                         1;
region of the invention. This sequence is not shown within the specification but is taken from Wipoweb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinuclectide; single nucleotide polymorphism; diffuse large = cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                          Length 3025,
                                         Sequence 3025 BP; 535 A; 0 C; 930 G; 1560 T; 0 U; 0 Other;
                                                                      tch
al Similarity 47.9%; Score 46; DB 9; Length 302
al Similarity 47.9%; Pred. No. 0.049;
162; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2180 TTGAGAGTTTTGTGGTGTTTTTTTTTTTTGTGGTGAT 2217
                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGAT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Becker E,
                                                                                                                                                                                                                                                                                                                   203 AGICGATTIATIGGATGATCCATICTICATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lymphoma; diagnosis; prognosis
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28-DEC-2001; 2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADE84157 standard; DNA; 3025
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                                                                                                                                                                                                                                                                                          2001
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                                                                              Query Match
Best Local
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The invention relates to a method of detecting and differentiating considers to the invention relates to a method of detecting and differentiating considers associated with at least cone gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between considering and non-methylated sample obtained from the subject with the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MDRI, CSNXZB, EGR4, AR, CDK4, RB2, CDC25A, GPID beta, MYDDI, CDH3, CK MYCLI, BERL1, APC, BCL2, CDH1, CDKNLA, CDKNZB, CDKNZB, CDKNZB, CGXZB, GRIZB, APARI, BAX, BAX OR HOXAS. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the cyclosine methylation state and or single nucleotide conditions such as diffuse large Bacell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular conditions under are useful. for detecting the methylation transcribers and or single nucleotide conditions the sequence conditions the use useful seases differentiation between subclasses, diagnosis, treating and/or expressents a nucleic acid of a pretreated genomic DNA derived from the above above mentices.
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Search completed: June 20, 2004, 01:58:58 Job time: 368.167 secs

Claim 26; SEQ ID NO 153; 448pp; English

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Submitted (17-SEP-1991) C. Gigot, Inst de Biologie Mol des Plantes,
Submitted di General Zimmer, 67084 Strasbourg Cedex, FRANCE
Location/Qualifiers
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/strain="Columbia"
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J. Mol. Biol. 225 (2), 569-574 (1992)
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Stochard DNA SEQUENCE FOR USE AS A REGULATOR REGION IN A CHIMERIC GENE USEFUL FOR TRANSFORMING PLANTS
PATENT: WO 9704114-A 7 06-FEB-1997;
RHONE POULENC ARROCHIMIE (FR)
Other publication FR 2736929
Location/Qualifiers
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/clone="C22"
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/wol_type="unassigned DNA"
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3227. .>3488
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GLHYYVAVFHRVVLRQPPKTNWKIHGVYATCFLLICLLSNAERRKKEYLEEGGDEGKK
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Rattus norvegicus, PIR2:A35723

Contains ABC transporters family signature AA580-594;ABC

transporters family signature AA1369-1383;ATF/GTP-binding

site motif A (P-loop) AA1247-1254

contains EST gb:N95877"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              john(16229. 16300,16394. 16679,16981. 17205,17341. 17
10775. 18129,18222. 18357,18433. 18811,19039. 19271,
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22750. 22983,23134. 23312)
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26723-26722; possibly related to subsequent gen"
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12287. 13642

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EPFTYDYDRNFLLTDWYHKSMSEKATGLASIPFKWVGEPQSLMIQGRGRFNCSNNLTT
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HYVEPPTYKOLLFVYSGETYSYLLKADQNPRRNYMITSSIVSRPATTPPATAVLNYYPN
HPRRRPPTSESSNIVPEWNDTRSRLAQSLAIKARRGFIHALPENSDKVIVLLNTONEV
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KRYNRVDPI KKNTVAVQPFGWTALRFRADNPGVWSFHCHI ESHFFMGMGI VFESGI DK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Jouce="strong similarity to L-ascorbate oxidase, Cucumis sativus, PIRI:KSKVAO
Contains Glycosyl hydrolases family 5 signature
AA384-39; Multicopper oxidases signatures
AA131-151; Multicopper oxidases signatures
AA540-560; Multicopper oxidases signatures
AA545-556; ProKaryotic membrane lipoprotein lipid
contains EST 90:A1994215.1, AA585817, A1996008.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Azabidopsis sequencing, project.

Direct Submission

Submission

Submission

Submission

Submission

Submission

MIOPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, B-mail:

lemcke@mips.biochem.mpg.de_mayer@mips.biochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/this frament has an overlap with ATCHRIV91 at the 5' end and an overlap with ATCHRIV93 at the 3' end.
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Volckaert, G., Grymonprez, B., Voet, M., Robben, J., Mewes, H.W.,
Lemcke, K. and Mayer, K.F.X.
                                                                                                                                                                                                                                                                                                                                           3 (bases 107578 to 112067)
Rose,M., Hempel,S., Entian,K.-D., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
Unpublished
                                                                                                                                                                          1 (bases 1 to 107700)
Murphy, G., Ridley, P., Hudson, S., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.
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    112067
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forganiam="penomic DNA"
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                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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chromosome="4"
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VERSION
KEYWORDS
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KMGARDLLALVATVVFRTALSNRLAKVQGFLFRAAFLRRADLFLRLISENIMLCFMLS
TLHSTSKYITGALSLRFRKILTKIIHSHYFENMVYYKISHVDGRITHPEQRIASDVPR
FSSELSDLILDDLTAVTDGILYAWRLCSYASPKYIFWILAYVLGAGTAIRNFSPSFGK
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Direct Submission

Submitted (21-SEP-1999) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, Cambridge
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 700 Norwich, UK,
E-mail: michael: Devan@bberc.ac.uk
On Sep 22, 1999 this sequence version replaced gi:4490734.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
Incation/Onalifiers
83675 TCTIGCTICGAAGTICTGTATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCG 83616
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Arabidopsis thaliana DNA chromosome 4, BAC clone T5J17 (ESSA
project).
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2. (bases 1 to 118267)

EU Arabidopsis sequencing, project.
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudioctyledons, core eudiocts,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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SSSSTKNOTKLAKTTIMOTSHKLNSTKSSSNTTKTSSELKKLNSGTKSTNSTSSIKKS ADLSKSSSNNKTTIKPPSSKLSSPPSEKKSQPSSKPVTKSKQSEKEIKPFWLDDEED BEPVSERFADLPTRSKSTISTSKNYTNKANKGITKÜRFWFYFFORNXAPFTIAS VOSTVFILVPLLLLVSLIFNRFKAYFSLUKTLIFIQIYLSITYESILCLSSLVTGTEPLK FLYATSSSTYVCLQILGTLGYVFYLLLLLMYLVLVFSTDCGLGLKVLGLAQTFVGFAK NatyvvavffrkvvlrQppktinwkihgvvatcfillicllsnaerrkkevlebeggdbegkk	2285424209 2981e = 11517.10"			join(4680628687,2858127246,2754827772,2790828105, 2824228696,2878928924,2900029078,2960629838, 2989330197,3027930411,3046830623,3078031002, 3108231190,3141231502,3177231939,32020, .32135,	11,3272932929,33101. 19)	/note="similarity to 70K peroxisomal membrane protein, Rattus norvegicus , PIR2:A35723 Contains AEC transporters family signature [LSLGROORIGMARTE] [15.4780081494951.]	/codon_start=1 /product="putantyoe protein"	/db_xref="f01+499736" /db_xref="f01+499736" /db_xref="f02+1098MR8"	/ no_xver="s=rand=server" / no_xver="s=rand=server" / no_xver="s=rand=server" / reassatation="noscontenterers" / reassatation="noscontenterers" / reassatation="noscontenterer" / reassatation	AMGARULLALVATVVEKTALDSKLARVOGFLERARFLERAFLERAFLEBRIMLOFFLIS TLHSTDSKYTTGALSLEFERILTKITISHYFENMVYYKISHVDGRITHPBQRIASDVPR FSSELSDLILDDLIAVTDGILYAMRLCSYASPKYTFWILAYVLGAGTAIRNEFSPSFGK IMSYEOOT FORVOOTHESTGIA FVACTOMPSPSELIONERALIAUTHENDERA	WFGMTQDFLLKYLGATVAVII.IEPFBGHLRPDDSTLGRAEMLSNIRHTRYISLF QALGTLSISSRRLNRLSGYADRIHELMAVSRELSGDDKSSFQRNRSRNYLSEANYVEF	SDVKVVTTGYNLVEDELTLRYBOGSNLLITGGLWPLVSGHIVKROYGEDLKNE FYVP QRPYMAVGTLRDQLIYPLTGGQESELLTEIGMVELKNVSILVSLFYTRMVDLEYLLD RYQPBKBVNWDDELSLGBQQLGMARLFYHKPKRAILDBCTSAYTTDMERFAAKVRA	MGTSCITI SERPALVAFHDVVLSLDGEGGWSVHYKRDDSALLTDAEIDSVKSSDTDRQ NDAWVVQRAFAAARKVSAEVLFESATUSKAGSVQTQLIARSFVUDRSVFDPOT SQRALPSRVAAMLNVLLPWKFHLFCISTWLYKSSCADANIDIILLKTDHFIVTFOI	PTIFDKQGAQLLAVACLVVSRTLISDRIASLNGTTVKYVLEQDKAAFVRLIGLSVLÖS GASSIIAPSLRHLTQRLALGWRIRLTQHLLRNYLRNNAFYKVFHMSGNSIDADQRLTR DLEKLTADLSGLLTGWVKPSVDILWYVRYVGLISNICFMRGVAILYTYMLGLGFLRR	VAPDFGDLAGEEQQLEGKFRPTSSCLCRFWHERLNTHAESIAFFGGGRREKAVSFLIA LAIAAGFWYVIFESKLPEVNLELFYHLCDDGLFMSNVASLMVDKKFRALLDHSLMLLR KKWLYGILDDFVTKQLPNNVTWGLSLLYALEHKGDRALVSTQVKYLHVLYMMLLIPGE	LAHALKYLASVVSQSFRAFGDILBELHKKFLELSGGINNI FELDEFLDAGOSGYTSENQ ISRLDSQDLLSFSEVDIITPAQKLMASKLSCEIVSGKSLLVTGPNGSGKTSVFRVLRD INPTVCRLITKPSLDIKELGSGNGMFFVPQDRPYTCLGTLRDQIIYPLSKERAEKRAAK LYTSGRSGFRAGSIIDSHLKTTENVRLVYTI.RPDVGGWDATTWWFDIISIGROORIG	MVSLL	/number=1 26868. 26960	/gene="15-17.20" /mumber=1 2696127246	/gens="T5117.20" /mumber=2 2724727547	/gene="1501/.zo" /mumber=2 2754827772	/gene="T517.20" /number=3 2777327907
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Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
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Arabidopsis thaliana T-DNA flanking sequence, right border, clone
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AJ69263. GI:37942256

Arabidopsis thaliana (thale crees)

Arabidopsis thaliana

Busaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Anauvin,S., Bechirold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharmy,A.
T_DNA integration into the Arabidopsis genome depends on sequences
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plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
                                                                                                                                                                                                                                                       137 CTCAGGCGAAGAACAGGTATGATTGTATTGTAATTAGATCAAGGGTTTAGGTCTTTCCAT
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Pred. No. 4.3e-101;
0; Mismatches 3;
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                    Olek, A., Piepenbrock, C. and Berlin, K.
Method and nucleic acids for pharmacogenomic methylation analysis
Patent: WO 0202806-A 65 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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                                                                                                                                                                                                                                               18 TATGATTTGTTTGTAATTAGATCAGGGGTTTAGGTCTTTCCATTACTTTTAATGTTTTT
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Best Local Similarity 46.5%; Pred. No. 0.0061;
Matches 180; Conservative 0; Mismatches 207; Indels 0;
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                                                                                                                                                                                      Query Match
Best Local Similarity 46.5%; Pred. No. 0.0061;
Matches 180; Conservative 0; Mismatches 207; Indels 0;
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Diagnosis of diseases associated with cell signalling
Patent: WO 020807-A 119 10-JAN-2002;
Epigenomics AG (B)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      78 ICTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTT
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Sequence 119 from Patent WO0202807.
AX348661.
AX348661.1 GI:18614696
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ACCESSION
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Submitted (17-OCT-1990) Hishinuma F., Mitsubishi Kasei Institute of
Life Sciences, 11 Minamiooya Machida-shi, Tokyo 194, Japan
Location/Qualifiers
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X54850
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                                                                                         TCTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCCATTC 137
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77
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Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Genome organization of the linear plasmid, pSKL, isolated from Saccharomyces kluyveri
Mol. Genet. 226 (1-2), 97-106 (1991)
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558. ...1279
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Saccharomyces kluyveri
Saccharomyces kluyveri
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Hishinuma, F.
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mRNA mRNA

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complement (<11371. .11761)
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EKNLDDVSFNACVSLVFFTIYKDTEKKTLQIYIKDLVVVEIIKDELBIBLDKLSLAM"
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12013. ,13389
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                                                                                                                                                                                                                                                                                                                                                                                                                          xref="SPTREMBL:Q04306"
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RNA polymerase"
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7873. .>8387
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KKKENRY FDKQI EYDLQQY
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YIFNNFIDKLYTLKDIHTNCKCKEQPCPIRMYAKIALNGGGYGKFVOKPIDKEVYIVK
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LAYHFEIIRKLYTYTTDKIIKDIKQT"
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TSNFVIENKTNYKKILKNLKDNGWYHQBIKIKNKMEIGTIQRRELSRMYTYHYLKKIK
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IYRKRLQEDPIVEITKYNNEFNLEVEFDINNYEKVEKILKEWKSPYMPPVKPMĒISSS
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YFYKYLDIDSESSLEVPLKENIETDFGFDPNTVYGENELCEBYERKFFRSFEFNKGIE
                                                                                                                                                                                                                                                                                                                                                                                                   'note="unnamed protein product; ORF 2, has similarity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170. .7927
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                                                                                                                                                                                                                                                          complement (<1276. .4278) /note="ORF 2"
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/db Xref="taxon:32630"

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1.249.980-seq 03 60.001 949.980-seq 04 900.001

1.249.980-seq 05 1.200.001 1.549.980-seq 06 1.500.001

2.449.980-seq 07 1.800.001 2.749.980-seq 08 2.100.001

2.449.980-seq 07 1.800.001 2.749.980-seq 10 2.700.001

3.049.980-seq 01 3.000.001 3.749.980-seq 12 3.300.001

3.649.980-seq 13 3.000.001 3.749.980-seq 12 3.300.001

1.549.980-seq 19 1.500.001 1.249.980-seq 21 1.200.001

1.549.980-seq 19 1.500.001 2.449.980-seq 22 2.400.001

2.149.980-seq 21 2.700.001 2.449.980-seq 22 2.400.001

2.749.980-seq 22 2.700.001 3.649.980-seq 24 3.000.001

3.543.778"
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314 AGGGTTTTTCGAGTCAATTTTGCCCCTTTTGGTTATATCTGGTTCGATAACGATTCATCTG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54523 igigerirrangiratrakanakarrrrirraagarrirragiragirirrrrrrrr
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                                                                                                                              254 ITCTGIATAACCAGATTIGTCTGTGCGATTGTCATTACCTAGCCGTGTATCGAGAACT
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Diagnosis of known genetic parameters within the mhc
Patent: WO 0200932-A 24 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                       374 GATTAGGGTTTTAAGTGGTGACGTTTAGTATTCCAATTTCTTCAAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 49.6; DB 6; Length 3 Pred. No. 0.13; 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Sequence 24 from Patent W00200932.
AX344573 GI:18492459
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127; Conservative
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Best Local Si
Matches 127;
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SOURCE
ORGANISM
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ACCESSION
VERSION
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AUTHORS
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RDYNKLGRLKKGKIIDLSNIGIVDENATDIITWPETENLYSSKTLETTRTPRTFCKNI
                                                                                                                                                                                                                                                                                                                                                                                                                                   11290 İTGICTIGCĞĞCCATAĞATAĞTATAÇCAATCATCATTITTATTTÜĞĞÇĞTTĞTAAĞĞ 11231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 ATTCCAGTTTGAAAATAAACGTCCGTCTTTTAAGTTTGCTGGATCGATAAACCTGTGAAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 TTTTTCTGTTACTGTCTCCGCGATCTGATTTTACGACAATAGAGTTTCGGGTTTTGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               255 TCTGTATAACCAGATTTGTCTGTGTGCGATTGTCATTACCTAGCCGTGTATCGAGAACTA
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                                                                                                                                                                                                                                                                                                            Score 50.6; DB 8; Length 1
Pred. No. 0.099;
0; Mismatches 144; Indels
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 AIGAAAATCCCGAAITGACTGTTCAATTTCTTGTTAAATGC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA
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Sequence 14 from patent US 5670367.
1166494 1 GI:2724471
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                                                                                                                                                                                                                                                                                                            10.2%;
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Best Local Similarity 48.8
Matches 137; Conservative
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Danio rerio
Danio rerio
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopererygii, Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                             Olek.A., Piepenbrock,C. and Berlin,K.
Method and nucleic acids for pharmacogenomic methylation analysis
Patent: WO 0202806.A 2 10-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
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AL953898.20 GI:35763627
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/mol_type="unassigned DNA"
/db xracf="taxon:3260"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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9.9%; Score 49; DB 6; Length 17869;
Best Local Similarity 46.0%; Pred. No. 0.23;
Matches 210; Conservative 0; Mismatches 240; Indels
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Sequence 2 from Patent WO0202806.
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                                                       54703 AAİTITITITAGİLIAİTAĞAİĞIAAĞAİATİTIĞİTITGİTIĞİTİTİTAĞITITİTA 54762
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/mol_type="unassigned DNA"
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Sequence 78 from Patent WO0200928.
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locus_tag="PF14_0238"
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/chromosome="14"
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/rpt_type=tandem
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

EMS: SW: SWISSEROT; Tr:, TREMBL; WP:, WORWEPP: Information on the WORWEPP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived length of monoucleotide A/T runs and conserved TR repeats. Where length of monoucleotide A/T runs and conserved TR repeats.
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The secon repeat by the Recon repeat con every every every supplied (Zhirong Bao and Sean Eddy, submitted), and those
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                   Cambridgeshire, CB10 15A, UK. E-mail enquirtes:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 25, 2003 this sequence version replaced gi:35209226.
Submitted (27-SEP-2003) Wellcome Trust Sanger Institute, Hinxton,
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Pred. No. 0.19;
0; Mismatches 140; Indels 0;
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                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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Best Local Similarity 48.7
Matches 133; Conservative
        JOURNAL
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plasmodium falciparum 3D7
plasmodium falciparum 3D7
plasmodium falciparum 3D7
blasmodium falciparum 3D7

[bases 1 to 250029]
plasmodium, Alveolata; Apicomplexa; Haemosporida; Plasmodium.

[cardnor, M., Rail, N., Fung, E., White, O., Berriman, M., Hyman, R.W., James, K., Eisen, J.A., Rutherford, K., Solzberg, S.L., Craig, A., Kyene, V., Shallom, S.J., Suh, B., Peterson, J., Kyes, S., Chan, M.-S., Nene, V., Shallom, Suh, B., Peterson, J., Martin, D.M.A., Refalamb, A.H., Pranuholz, M., Ross, D.S., Ralph, S.A., McFadden, G.I., Cummings, L.M., Subramanian, G.M., Mungall, C., Venter, J.C., Carucci, D.J., Hoffman, S.L., Newbold, C., Davis, R.W., Fraser, C.M. and
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NILGENMSNIFEEDKELDLFSSFKDIFNNHKKKIKLJDYNKILNKSLYDNVENVDSLI
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I PYTSKEL YTYKEY SKKLDCNDLNKLSDEKETTKN I SNDLEL I KKEKKKKNDDTFFFI
SHNEKDKNYLFPYDHKGDDNYNDEDKNNLLPCDHI CDDNYNDEDKNNLLPCDHI CDDN
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YODENDELYKUDEGKIKODIYANDENDELYKNGGIKJODIYANDENDEKLYKYDOGKIKODI
IYNDENDELYKNDGKIKODIYANDENDMIJNSMESPERTKYIGNIKBNDKLLKYVWKE
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RGNFFEKKKTENDVKEI I KNI KARLGFYSNEESDSHDI KCLENDDDNDDDDNNDDNDD
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Nature 419 (6906), 498-511 (2002)
AB014820 250029 bp DNA linear INV 07-OCT-2002 Plasmodium falciparum 3D7 chromosome 14 section 5 of 13 of the
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Submitted (13-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
Location/Qualifiers
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Best Local Similarity 21.8
Matches 57; Conservative
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463 TCTTGTTAAATGCGCAGATCC 483 | : : | | : | | | | 129506 TYCMRCTAWTTYWWYATCTTC 129526

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Search completed: June 20, 2004, 03:45:49 Job time: 3467.42 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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sw model using search, nucleic nucleic ŏ June 20, 2004, 01:40:43; Search time 59.125 Seconds (without alignments) 3923.374 Million cell updates/sec Run on:

US-09-000-062-6 418

1 tgaggtacgattcttcgatc......taatttgttgaacagatccc Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

682709 segs, 277475446 residues Searched:

1365418 hits satisfying chosen parameters: Total number of

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents NA:\*

1. /ogn2 = 6/ptodata/2/ina/5A\_COMB.seq:\*

2. /cgn2 = 6/ptodata/2/ina/5B\_COMB.seq:\*

3. /cgn2 = 6/ptodata/2/ina/6A\_COMB.seq:\*

3. /cgn2 = 6/ptodata/2/ina/6B\_COMB.seq:\*

5. /cgn2 = 6/ptodata/2/ina/PcTUS\_COMB.seq:\*

5. /cgn2 = 6/ptodata/2/ina/PcTUS\_COMB.seq:\*

5. /cgn2 = 6/ptodata/2/ina/PcTUS\_COMB.seq:\* 47 M 4 M 9 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Appli	Appli	l, Appl	4, Appl	3, Appl	, Appl	l, Appl	6, Appl	7, Appl	, Appl	8, Appl	1, Appl	, Appl	Appli	Appl	2, Appl	3, Appl	, Appl	Appli	9, Appl	0, Appl	8, Appl	813, Ap	1, Appl	Appli	2100, Ap	40, Appl
	Description	Sequence 6,	Sequence 2,	Sequence 41	m	N	Sequence 55	Sequence 21	α	Sequence 37	Sequence 63	m	9	Sequence 2(	Sequence 3,	Sequence 33	Sequence 62	H	Sequence 85	Sequence 7,	N	Ŋ	w	N	Н	Sequence 5,		
SUMMARIES		09-000-062-6	07-867-106-2	10-204-708-41	10-204-708-34	10-204-708-23	9	09-627-122-21	10-204-708-86	10-204-708-37	2	10-204-708-38	10-204-708-61	US-10-204-708-20	09-751-389-3	10-204-708-33	US-10-204-708-62	$^{\circ}$	2	09-078-294-7		10-204-708-50	08-956-171E-38	09-621-976-2813	US-10-204-708-11	09-417-485D-5	US-09-134-001C-2100	JS-10-204-708-40
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1, 70, 71, 3,	Sequence 14, Appl Sequence 32, Appl Sequence 10, Appl Sequence 10, Appl Sequence 45, Appl	30, 72, 1017 80,	Sequence 1, Appli Sequence 42, Appl
US-09-790-988-1 US-10-204-708-70 US-10-204-708-71 US-09-734-674-3 US-10-204-708-14	US-08-232-463-14 US-10-204-708-32 US-10-204-708-16 US-10-204-708-45	US-10-204-708-30 US-10-204-708-30 US-10-204-708-72 US-09-134-001C-1017 US-10-204-708-80	US-09-056-075-1 US-10-204-708-42
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ALIGNMENTS

General No. 6338961

Fatent No. 6338961

GREEAL INFORMATION:
APPLICANT: DEROSE, Richard
APPLICANT: CHAUBET, Nicole
APPLICANT: CHAUBET, Nicole
TITLE OF INVENTION: ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY
TITLE OF INVENTION: TRANSPORMATION OF PLANTS
TITLE OF INVENTION: ELEMBNT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE
TITLE OF INVENTION: 1990-95-29
TITLE REPERBNCE: 022669-453
CURRENT APPLICATION NUMBER: US/09/000,062
CURRENT FILING DATE: 1998-05-29
EARLIER PILING DATE: 1998-07-17
EARLIER PILING DATE: 1998-07-17
SARLIER PILING DATE: 1995-07-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6

; TYPE: DNA ; ORGANISM: Zea mays US-09-000-062-6

ô 9 1 TGAGGTACGATTCTTCGATCCTCTTTGATTTTTCCTGGAAATATTTTTCGGTGATCGTGA Gaps . 0 Indels Query Match 100.0%; Score 418; DB 4; L Best Local Similarity 100.0%; Pred. No. 1.8e-102; Matches 418; Conservative 0; Mismatches 0; ð

Length 418;

09 readdracearretrecarecrerrrearrirecredaaararrrregergareerea g

120 120 180 ccarrarcrrcrrcccccaarcarcrrcccraraaagarrragcrragagargaa 180 AACTACTGGAATCGCTCGATAGGTGGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGG AACTACTGGAATCGCTCGATAGGTGGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGG CCATTATCTTGTTTCTTCGCCGAATGATCTTCCGTATAAAGATTTTAGGTTAGAGATGAA 61 61 121 121 ઠ 셤 임 8

240 240 TAGITITICACATGIGIAAAIAGAIIGITCITATICGGCGAIIGGITGAITAGGGITTIGAT 300 TCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCTCTGAAATTCTCGA TCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTAGAATCTCTGAAATTCTCGA 181 181 241 Д ₹ ð

TAGITITICACATGIGIAAATAGATIGITCITATICGGCGATIGITGATIAGGGITITIGAT 300

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321 AATTAGGGATTITCTTTGGTTTTGTGTTGATCTTACATTCCTGCAATTGAATACG 380
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Sequence 34, Application US/10204708
Batent No. 6677731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEBRIBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
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                                                                                                                                                              2306 ATTTATTGTAATTCATTTTATTTATT 2332
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                                                                                                                   381 TATGGATCTAAATCTTGTTAATTTGTT
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ORGANISM: Artificial Sequence
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US-10-204-708-41
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                           301 TITCTIGATTATGCGATTGCAATTAGGGATTTTCTTTGTGTTTGTGTTGATCTTACGATA 360
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TITCTIGATTATGCGATTGCAATTAGGGATTTTCTTTGGTTTTGTGTTGATCTTACGATA 360
                                                                                          361 CATTCCTGCAATTGAATACGTATGGATCTAAATCTTGTTAATTTGTTGAACAGATCCC 418
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris STREET: One Liberty Place 46th Floor CITY: Philadelphia
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                                                                                                                                                                                                                                          Sequence 2, Application US/07867106
Patent No. 5389526
GENERAL INPORMATION:
APPLICANT: Cland, Martin B
APPLICANT: Cland, Andy C M
APPLICANT: Cland, Andy C M
APPLICANT: Cland, Reith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostellum
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/867,106
FILLIGO DATE: 19920625
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DCT/AU90/00530
FILLING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: ATTORNEY DCT/AU90/00530
FILLING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFRENCE/DOCKET NUMBER: RICE-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPRAX: 215-568-3100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5852 base pairs
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
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2378..5038
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
Matches 105; Conserv
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LOCATION:
FEATURE:
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FEATURE:
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Sequence 41, Application US/10204708

Sequence 41, Application US/10204708

Sequence 41, Application US/10204708

Sequence 41, Application US/10204708

Sequence 41, Application US/10204731

SERENTA INFORMATION:
APPLICANT: PERENBROCK, Christian
APPLICANT: PERENBROCK, Christian
APPLICANT: PERENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REPRENCE: 5013.1012

CURRENT APPLICATION NUMBER: DS/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR PELING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PELING DATE: 2000-04-06

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

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PRIOR FILING BATE: 2000-06-30

PRIOR FILING BATE: 2000-06-30

PRIOR FILING BATE: 2000-09-01 2246 TTTTTTTTATTTTTTTTTTTTTTTTTTTTTTTCCCACACACTTTCATTTTATTTT 2305 7905 TIGIATITITITIAGITITITIGGITATIATIGITITIATITIGITITITIGIATIGAATI 7964 262 143 AATGATCTTCCGTATAAAGATTTTAGGTTAGAGATGGAATCGTATAGCTAGATTTCATCAC 202 263 ATTGTTCTTATTCGGCGATTGTTGATTAGGGTTTTTGATTTTCTTGATTATGCGATTGCAA 322 203 CAGATAGTTTCTTTGTCTAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATTAG Gaps

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Query Match
Best Local Similarity
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US-10-204-708-55
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Sequence 23, Application US/10204708

Patent No. 6677731

SERERAL INFORMATION:

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, MILL

TITLE OF INVENTION: Dy Assessing DNA Methylation

001-04-06

PRIOR PELLING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR PELLING DATE: 2000-04-07

PRIOR PELLING DATE: 2000-04-07

PRIOR PELLING DATE: 2000-04-07

PRIOR FILING DATE: 2000-09-01

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

SEQ ID NO 23

LENGTH: 11049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.6%; Score 40.2; DB 4; Length 5 Best Local Similarity 47.8%; Pred. No. 0.12; Matches 117; Conservative 0; Mismatches 128; Indels
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: CFT/FF01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FLING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-31
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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US-10-204-708-23
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APPLICANT: OLEY, Alexander
APPLICANT: OLEY, Alexander
APPLICANT: PEREBRENGCK, Christian
APPLICANT: PEREBRECK, Christian
APPLICANT: PEREBRECK, Christian
APPLICANT: PEREBRECK, Christian
APPLICANT: PEREBRECK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DA Assessing DNA Methylation
FILER REPERENCE: 5013.102
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DCT/EPO1/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR PELING DATE: 2000-04-06
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                        71 ATCGCTCGATAGGTGGTACGAAATTAGGCGAGATTAGTTTCTATTCTTGGCCATTATCTT
                                                                    ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-204-708-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                     Length 11049;
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                                                                                                                                                                  Score 40.2; DB 4; Length 1 Pred. No. 0.15; 0; Mismatches 223; Indels
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Pred. No. 0.21;
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Patent No. 6677731
ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                     Query Match
Best Local Similarity 43.8%;
Matches 174; Conservative
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CURRENT FILING DATE: 2003-05-06

PRIOR APPLICATION NUMBER: PCT/BP01/03971

PRIOR PILING DATE: 2001-04-06

PRIOR FILING DATE: 2001-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR APPLICATION NUMBER: DE 1003529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 98

LENGTH: 11050
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ORGANISM: Artificial Sequence
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                                             209 GTTTCTTTGTCTAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTT 268
                                                                                                                                         269 CTTATTCGGCGATTGTTGATTAGGGTTTTGATTTTCTTGATTATGCGATTGCAATTAGGG 328
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Sequence 86, Application US/10204708
Patent No. 6677731
GENERAL WINFORMATION:
GENERAL PREPRIEDRY: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PERPRIBENCE, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/09627122

Patent No. 6472521

GENERAL INFORMATION:
APPLICANT: Unlamn, Eugen
APPLICANT: Greiner, Beate
APPLICANT: Greiner, Beate
APPLICANT: Greiner, Beate
APPLICANT: Grew, Gislinde
APPLICANT: Grewerdel, Marc
TITLE OF INVENTION: EXPRESSION
FILE REPRENCE: 074811678
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT APPLICATION NUMBER: US/09/627,122
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
0; Gaps
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64; Indels
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0; Mismatches
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78; Conservative
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LENGTH: 5340
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Matches
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Sequence 37, Application US/10204708

Sequence 37, Application US/10204708

Ratent No. 6677731

SERERAL INFORMATION:
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
APPLICANT: DIEBENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE OF INVENTION: DY Assessing DNA Methylation
CURRENT FILING DATE: 2003-05-06
PRIOR PELLING DATE: 2001-04-06
PRIOR PELLING DATE: 2000-04-06
PRIOR PELLING DATE: 2000-04-06
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE
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                                                                                                                                                                                                                                                                                                                                         Gaps
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                   Length 11050;
                                                                                                                                                                                     Query Match
9.4%; Score 39.2; DB 4; Length 1
Best Local Similarity 46.9%; Pred. No. 0.27;
Matches 122; Conservative 0; Mismatches 138; Indels
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427 TITITIAIAGITITITICGAITAGIGITITITITITIGIATITAAAGICGITITITAITITI 486
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                                                                                                                                    388 CTAAATCTTGTTAATTTGTT 407
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Patent No. 6677731
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US-10-204-708-38
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APPLICANT: DIESENBROCK, Christian
APPLICANT: DIESELIN, Wint
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-04-07
PRIOR PRILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 63
LENGTH:: 5562
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                                                                                                                                                                                                                             102 GATTAGITTCTATTCTTGGCCATTATCTTGTTTCTTCGCCGAATGATCTTCCGTATAAAG 161
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                                                                                                                                                                                                                                                                                                                  162 ATTITAGGITAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCTTTGTCTA
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                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.2%; Score 38.4; DB 4; Length 5562; Best Local Similarity 49.5%; Pred. No. 0.37; Matches 99; Conservative 0; Mismatches 101; Indels 0
                                                                                                                                  Length 5501
                                                                                                                               Score 39; DB 4; Length 550
Pred. No. 0.26;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 63, Application US/10204708
Patent No. 6677731
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                  Query Match
Best Local Similarity 49.8%;
Matches 126; Conservative
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BELLIN, Kure
ITILE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
FILE SEPERBROES: 5013-1012
CURRENT APPLICATION NUMBER: US/10/204,708
FRIOR APPLICATION NUMBER: US/10/204,708
PRIOR PILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 1001973.8
PRIOR APPLICATION NUMBER: DE 1001973.8
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 38
LENGTH: 5501
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328 GATTITCTTIGGITTIGGITTIGALCTIACGATACATICCTGCAATIGAATACGTAIGGAI 387
                                                                 Sequence 61, Application US/10204708
Patent No. 657731
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIERPARROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 TTTCTTTGTCTAGAATCTCTGAAATTCTCGATAGTTTTCACATGTGTAAATAGATTGTTC
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49.48;
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        Best Local Similarity 49.49
Matches 126; Conservative
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Best Local Similarity 55.2<sup>5</sup>
Matches 74; Conservative
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ORGANISM: Human
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SEQ ID NO 3
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US-09-751-389-3/c
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Sequence 20, Application US/10204708

Sequence 20, Application US/10204708

Sequence 20, Application US/10204708

Sequence 20, Application

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: PIEPENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: by Assessing DNA Methylation

FILE REFERENCE: 5013.102

CURRENT APPLICATION NUMBER: US/10/204,708

CURRENT FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PELING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR PELING DATE: 2000-04-06

PRIOR PELING DATE: 2000-04-06

PRIOR APPLICATION NUMBER: DE 10013529.7

PRIOR APPLICATION NUMBER: DE 10043826.1

PRIOR APPLICATION NUMBER: DE 10043826.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192 İGAĞGĞAİAAAİTĞİTİTTĞGIĞĞIAĞTIĞIATTAĞITITAİTTİTİTİATIAATAAİĞISI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 AGGGTTTTGATTTTCTTGATTATGCGATTGCGATTAGGGATTTTCTTTGGTTTTGTGTT 348
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.1%; Score 38.2; DB 4; Length 6801; Best Local Similarity 50.8%; Pred. No. 0.45; Matches 91; Conservative 0; Mismatches 88; Indels 0
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TITLE OF INVENTION: by Assessing DNA Methylation FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT TILING DATE: 2003.05.06
PRIOR PILING DATE: 2001.04.06
PRIOR PILING DATE: 2001.04.06
PRIOR PILING DATE: 2000.04.06
PRIOR FILING DATE: 2000.04.06
PRIOR PILING DATE: 2000.04.07
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR PILING DATE: 2000.04.07
PRIOR APPLICATION NUMBER: DE 10035229.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000.06.30
PRIOR FILING DATE: 2000.06.30
PRIOR FILING DATE: 2000.06.30
PRIOR FILING DATE: 2000.06.30
PRIOR FILING DATE: 2000.06.30
PRIOR FILING DATE: 2000.06.30
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PRIOR FILING DATE: 2000.06.30
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ORGANISM: Artificial Sequence
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APPLICANT GUEGLER, Karl et al
TITLE OF INVENTION: TESCLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE REFERENCE: CLOU1067
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
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                                                                                             155 TATAAAGATTTTAGGTTAGAGATGAATCGTATAGCTAGATTTCATCACCAGATAGTTTCT
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                                    1; Gaps
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Pred. No. 1.8;
0; Mismatches 60; Indels 0
Pred. No. 0.45;
0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-204-708-33
US-10-204-708-33, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: DIEDEK, BLEARMER
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(786431)
; OTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09751389; Patent No. 6630334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455555 AATCAAAGGATAAA 455542
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us-09-000-062-6.rni

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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: by Assessing DNA Methylation
FILE REPERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT FILING DATE: 2003-05-06
PRIOR PILING DATE: 2001-04-06
PRIOR PILING DATE: D10019058.8
PRIOR FILING DATE: D2000-04-06
PRIOR PLING DATE: D200-04-06
PRIOR PLING DATE: D10019058.8
PRIOR PLING DATE: D10019058.8
PRIOR PLING DATE: D10019058.8
PRIOR PLING DATE: D100-04-07
PRIOR PLING DATE: D100-04-07
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PRIOR PLING DATE: D100-04-07
PRIOR PLING DATE: D100-03-01
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PRIOR PLING DATE: D100-04-06-01
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PRIOR PLING DATE: D100-04-06-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANSM: Artificial Sequence
FRATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.0%; Score 37.8; DB 4; Length 5455;
Best Local Similarity 53.8%; Pred. No. 0.54;
Matches 78; Conservative 0; Mismatches 67; Indels 0
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3799 GTTATTAATTTTTTAAGTTTTTA 3823 354 TACGATACATTCCTGCAATTGAATA 378 ઠે g

3679 hrrhmannhardaganharmannharminnharminnharmaganhagarahasharmaga 3738

234 TICTCGATAGTITTCACATGTGTAAATAGATTGTTCTTATTCGGCGATTGTTGATTAGGG 293

0; Gaps

3739 ririrariririrararırıradarırdaadgargasiriririririsararırırıradasırı 3798

294 TITIGATITICTICATIATGCGATTGCCAATTAGGGATTTTCTTTGGTTTTTGATCT 353

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ò g Search completed: June 20, 2004, 05:03:40 Job time: 61.125 secs